**BLASTP 2.2.9 [May-01-2004]**Reference :

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1088011356-16594-155894407553.BLASTQ4

Query=

(532 letters)

Database: All non-redundant GenBank CDS

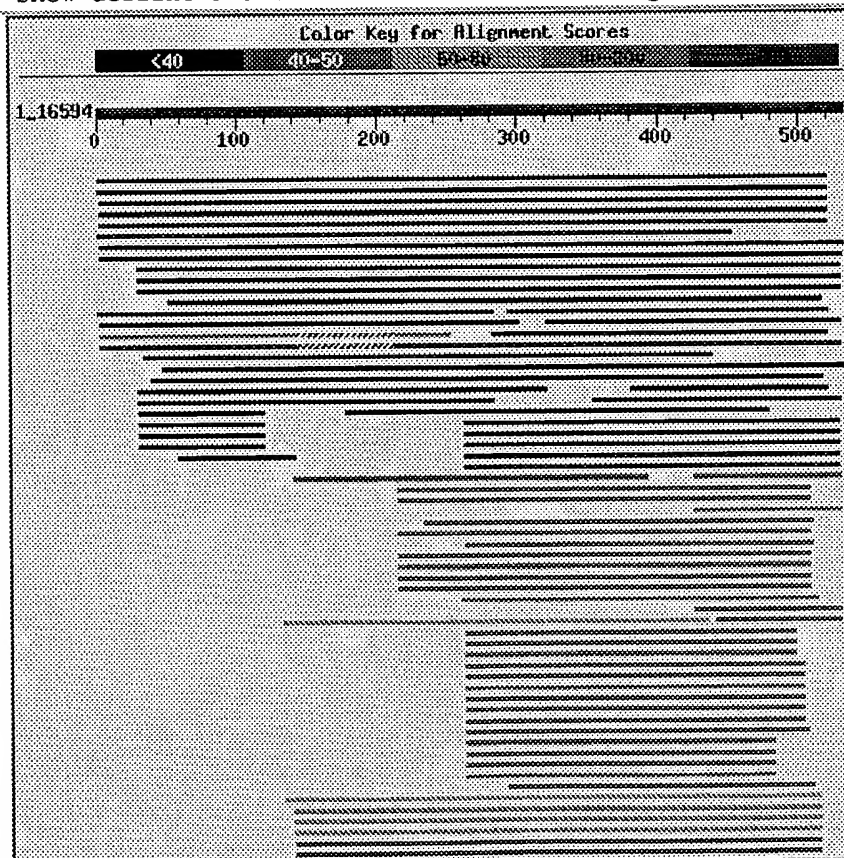
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
1,866,121 sequences; 619,474,291 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 103 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:				Score	E	
				(bits)	Value	
gi 40255141 ref NP_060841.3		chondroitin beta1,4 N-acetylga...		1075	0.0	■
gi 22852208 dbj BAC16217.1		beta-1,4-N-acetylgalactosaminy...		1074	0.0	■
gi 26348685 dbj BAC37982.1		unnamed protein product [Mus mu...		1002	0.0	
gi 31559877 ref NP_766341.2		RIKEN cDNA 4732435N03; beta1,4...		1001	0.0	
gi 26324624 dbj BAC26066.1		unnamed protein product [Mus mu...		1001	0.0	
gi 9651083 dbj EAB03554.1		hypothetical protein [Macaca fas...		915	0.0	
gi 34877724 ref XP_224757.2		similar to chondroitin beta1,4...		828	0.0	
gi 47219910 emb CAF97180.1		unnamed protein product [Tetrao...		720	0.0	
gi 24429592 ref NP_061060.3		chondroitin beta1,4 N-acetylga...		665	0.0	
gi 31560032 ref NP_084441.3		chondroitin sulfate GalNAcT-2 ...		659	0.0	
gi 26386533 dbj EAB31761.2		unnamed protein product [Mus mu...		657	0.0	
gi 47227595 emb CAG09592.1		unnamed protein product [Tetrao...		577	e-163	
gi 38174240 gb AAH60772.1		ChGn protein [Homo sapiens]		557	e-157	
gi 26340498 dbj BAC33912.1		unnamed protein product [Mus mu...		532	e-150	
gi 7023813 dbj BAA92093.1		unnamed protein product [Homo sa...		523	e-147	
gi 20072996 gb AAH26599.1		4732435N03Rik protein [Mus muscu...		494	e-138	
gi 34858369 ref XP_232316.2		similar to chondroitin beta1,4...		486	e-136	
gi 47216537 emb CAG04715.1		unnamed protein product [Tetrao...		485	e-135	
gi 31198419 ref XP_308157.1		ENSANGP00000021559 [Anopheles ...		382	e-105	
gi 34365000 emb CAE46036.1		hypothetical protein [Homo sapi...		361	2e-98	
gi 24652379 ref NP_610567.1		CG12913-PA [Drosophila melanog...		351	2e-95	■
gi 11360289 pir T46919		hypothetical protein DKFZp762L037.1...		317	5e-85	
gi 18677088 dbj EAB85092.1		unnamed protein product [Homo s...		317	5e-85	
gi 34365310 emb CAE45982.1		hypothetical protein [Homo sapi...		314	3e-84	
gi 37805317 gb AAH60159.1		Galnact2 protein [Mus musculus]		264	4e-69	
gi 47201472 emb CAF87906.1		unnamed protein product [Tetrao...		221	3e-56	
gi 37573674 dbj BAC98832.1		chondroitin sulfate synthase [H...		207	5e-52	
gi 42657278 ref XP_373440.2		chondroitin sulfate synthase 3...		207	5e-52	
gi 41529141 emb CAE17326.1		chodroitin synthase 2 [Homo sap...		207	6e-52	
gi 27681143 ref XP_225912.1		similar to carbohydrate (chond...		206	1e-51	
gi 28411190 emb CAD43233.1		chondroitin synthase 2 [Homo sa...		206	1e-51	
gi 7959793 gb AAF71068.1		PRO0082 [Homo sapiens]		195	2e-48	
gi 38086850 ref XP_194358.2		similar to mKIAA0990 protein [...		192	2e-47	
gi 37360174 dbj BAC98065.1		mKIAA0990 protein [Mus musculus]		192	2e-47	
gi 18606381 gb AAH23112.1		Galnact2 protein [Mus musculus]		191	3e-47	
gi 47086685 ref NP_997843.1		carbohydrate (chondroitin) syn...		187	5e-46	
gi 47213615 emb CAF95956.1		unnamed protein product [Tetrao...		186	9e-46	
gi 40789012 dbj BAA76834.2		KIAA0990 protein [Homo sapiens]		186	9e-46	
gi 15617453 dbj BAB64936.1		chondroitin synthase [Homo sapi...		186	1e-45	
gi 31542309 ref NP_055733.2		carbohydrate (chondroitin) syn...		185	2e-45	
gi 37182181 gb AAQ88893.1		CHSY1 [Homo sapiens]		185	2e-45	
gi 34857503 ref XP_218759.2		similar to carbohydrate (chond...		183	7e-45	
gi 41210270 ref XP_210054.3		similar to dJ341D10.1 (novel p...		174	3e-42	
gi 48139301 ref XP_396991.1		similar to chondroitin synthas...		174	3e-42	
gi 42662609 ref XP_378128.1		similar to dJ19N1.1 (novel pro...		149	2e-34	■
gi 31158517 gb AAO85275.1		chondroitin synthase-like protei...		136	1e-30	
gi 45555191 ref NP_996440.1		CG9220-PC [Drosophila melanoga...		136	1e-30	
gi 45555180 ref NP_996439.1		CG9220-PB [Drosophila melanoga...		135	2e-30	
gi 31158514 gb AAO85273.1		chondroitin disaccharide polymer...		134	6e-30	
gi 31044074 dbj BAC76780.1		chondroitin synthase [Caenorhab...		134	6e-30	
gi 31158515 gb AAO85274.1		chondroitin disaccharide polymer...		134	6e-30	
gi 17509239 ref NP_492630.1		chondroitin disaccharide polym...		134	7e-30	
gi 33300399 emb CAE17977.1		C. elegans SQV-5 protein (corre...		133	9e-30	

gi 39595217 emb CAE60254.1	Hypothetical protein CBG03828 [...]	129	2e-28
gi 31200511 ref XP_309203.1	ENSANGP00000005393 [Anopheles ...]	122	2e-26
gi 34867122 ref XP_342818.1	similar to chondroitin betal,4...	100	1e-19
gi 38566700 ref NP_942585.1	beta 1,4-N-acetylgalactosaminy...	94	7e-18
gi 21757529 dbj EAC05141.1	unnamed protein product [Homo s...	91	6e-17
gi 38566692 ref NP_775864.2	beta 1,4-N-acetylgalactosaminy...	91	6e-17
gi 47077041 dbj BAD18454.1	unnamed protein product [Homo s...	91	8e-17
gi 34861210 ref XP_219477.2	similar to hypothetical protei...	87	1e-15
gi 24416540 gb AAH38881.1	BC038881 protein [Mus musculus]	87	1e-15
gi 40789265 ref NP_848632.2	betal,4-N-acetylgalactosaminy...	86	2e-15
gi 46275756 dbj BAD15101.1	betal,4-N-acetylgalactosaminy...	86	2e-15
gi 16553708 dbj BAB71566.1	unnamed protein product [Homo s...	85	3e-15
gi 9229926 dbj EAB00632.1	Not6 [Ciona intestinalis]	84	1e-14
gi 47210467 emb CAF94230.1	unnamed protein product [Tetrao...	74	9e-12
gi 47217479 emb CAG10248.1	unnamed protein product [Tetrao...	69	3e-10
gi 37181931 gb AAQ88769.1	RASL651 [Homo sapiens]	67	8e-10
gi 47215238 emb CAG01130.1	unnamed protein product [Tetrao...	65	3e-09
gi 27545323 ref NP_078812.2	chondroitin polymerizing facto...	65	4e-09
gi 12053139 emb CAB66748.1	hypothetical protein [Homo sapi...	64	7e-09
gi 10439162 dbj EAB15449.1	unnamed protein product [Homo s...	60	1e-07
gi 39644837 gb AAH08878.2	CHPF protein [Homo sapiens]	60	2e-07
gi 23594326 ref XP_129886.2	DNA segment, Chr 1, Brigham & ...	59	4e-07
gi 48525359 ref NP_001001565.1	chondroitin polymerizing fa...	59	4e-07
gi 27685255 ref XP_237306.1	similar to chondroitin polymer...	57	1e-06
gi 47224136 emb CAG13056.1	unnamed protein product [Tetrao...	53	2e-05
gi 28972740 dbj BAC65786.1	mKIAA1402 protein [Mus musculus]	46	0.002
gi 34853978 ref XP_216063.2	similar to mKIAA1402 protein [...]	45	0.003
gi 18043971 gb AAH19714.1	2010209012Rik protein [Mus muscu...	45	0.004
gi 17554378 ref NP_498934.1	putative protein, with a coile...	42	0.031
gi 32565140 ref NP_871671.1	putative cytoplasmic protein, ...	42	0.049
gi 39585100 emb CAE62751.1	Hypothetical protein CBG06915 [...]	41	0.076
gi 19922240 ref NP_610946.1	CG8536-PA [Drosophila melanoga...	40	0.17
gi 34857950 ref XP_227406.2	similar to Lbcl1 protein [Ratt...	39	0.24
gi 28958144 gb AAH47275.1	Similar to RIKEN cDNA 2010209012...	39	0.32
gi 5305592 gb AAD41721.1	N-acetylglucosamine galactosyltra...	39	0.34
gi 26006191 dbj BAC41438.1	mKIAA0651 protein [Mus musculus]	39	0.36
gi 47271404 ref NP_032513.2	rho/rac guanine nucleotide exc...	39	0.37
gi 13879244 gb AAH06589.1	Rho/rac guanine nucleotide excha...	39	0.37
gi 29421290 gb AAO59307.1	kinesin [Gibberella moniliformis]	39	0.44
gi 15792460 ref NP_282283.1	putative two-domain glycosyltr...	38	0.61
gi 47227208 emb CAG00570.1	unnamed protein product [Tetrao...	37	1.2
gi 40353014 gb AAH64509.1	CSGlcA-T protein [Homo sapiens]	37	1.3
gi 42657991 ref XP_376724.1	KIAA1402 protein [Homo sapiens...	37	1.4
gi 48717495 ref NP_061888.1	chondroitin sulfate glucuronyl...	37	1.4
gi 7243185 dbj BAA92640.1	KIAA1402 protein [Homo sapiens]	37	1.4
gi 45383942 ref NP_990534.1	beta-1,4-galactosyltransferase...	37	1.6
gi 24372098 ref NP_716140.1	NAD(P)H-flavin reductase [Shew...	37	1.6

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|40255141|ref|NP_060841.3| chondroitin betal,4 N-acetylgalactosaminyltransf
sapiens]

gi|19352192|dbj|BAB85992.1| chondroitin betal,4 N-acetylgalactosaminyltransf
sapiens]

gi|37182006|gb|AAQ88806.1| MMVR656 [Homo sapiens]

Length = 532

Score = 1075 bits (2780), Expect = 0.0

Identities = 521/521 (100%), Positives = 521/521 (100%)

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 Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180
 Sbjct: 121 LAFLHSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180

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Query: 241 LFRPFSPIMKVKNEKLNMANNTLINVIVPLAKRVDKFRQFMQNFREMCI EQDGRVHLTVVY 300
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Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLI VVRTPV RGLFHLWHEKR 480
 Sbjct: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLI VVRTPV RGLFHLWHEKR 480

Query: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521
 Sbjct: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521

 >gi|22852208|dbj|BAC16217.1| beta-1,4-N-acetylgalactosaminyltransferase [Homo
 Length = 532

Score = 1074 bits (2777), Expect = 0.0

Identities = 520/521 (99%), Positives = 520/521 (99%)

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 Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180
 Sbjct: 121 LAFLHSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240
 Sbjct: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240

Query: 241 LFRPFSPIMKVKNEKLNMANNTLINVIVPLAKRVDKFRQFMQNFREMCI EQDGRVHLTVVY 300
 Sbjct: 241 LFRPF PIMKVKNEKLNMANNTLINVIVPLAKRVDKFRQFMQNFREMCI EQDGRVHLTVVY 300

Sbjct: 241 LFRPFGPIMKVKNEKLNMANNTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360
 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD

Sbjct: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPPEQQQLVIKKETGFWRD 420
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPPEQQQLVIKKETGFWRD

Sbjct: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPPEQQQLVIKKETGFWRD 420

Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKR 480
 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKR

Sbjct: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKR 480

Query: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521
 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR

Sbjct: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521

☐ >gi|26348685|dbj|BAC37982.1| unnamed protein product [Mus musculus]
 Length = 530

Score = 1002 bits (2590), Expect = 0.0

Identities = 477/521 (91%), Positives = 496/521 (95%), Gaps = 4/521 (0%)

Query: 3 MVRRLGLAWISRVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAVLQ 62
 MVRRLGL WISRVV+LLVLLCCAISVLYMLACTPKGD+EQL LPRAN PTGK+GYQAVLQ

Sbjct: 1 MVRRLGLGWISRVVILLVLLCCAISVLYMLACTPKGDQEQGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL

Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 180
 LAF L QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL

Sbjct: 119 LAFLRQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDEL 178

Query: 181 VEAIESALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240
 VEAIESALE+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTLYELTFKGDHKHEF+RL+

Sbjct: 179 VEAIESALESLSNPVLESSPHQRPYTAADFIEGIYRTERDKGTLYELTFKGDHKHEFQRLV 238

Query: 241 LFRPFGPIMKVKNEKLNMANNTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300
 LFRPF PIMKVK EKLN+ANTLINVIVPLA+RVDKFR FMQNFREMCI+QDGRVHLTVVY

Sbjct: 239 LFRPFGPIMKVKKEKLNLANNTLINVIVPLARRVDKFRHFMQNFREMCIQDGRVHLTVVY 298

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360
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Sbjct: 299 FGKEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 358

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPPEQQQLVIKKETGFWRD 420
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG+IYGHHDVAPP L QQLVIKKETGFWRD

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Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKR 480
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Sbjct: 419 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKH 478

Query: 481 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521
 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR

Sbjct: 479 CMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 519

☐ >gi|31559877|ref|NP_766341.2| RIKEN cDNA 4732435N03; beta1,4 N-acetylgalactosa
 [Mus musculus]

gi|26329203|dbj|BAC28340.1| unnamed protein product [Mus musculus]
 Length = 530

Score = 1001 bits (2588), Expect = 0.0

Identities = 476/521 (91%), Positives = 496/521 (95%), Gaps = 4/521 (0%)

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 MVRRLGL WISRVV+LLVLLCCAISVLYMLACTPKGDE+EQL LPRAN PTGK+GYQAVLQ
 Sbjct: 1 MVRRLGLGWISRVVILLVLLCCAISVLYMLACTPKGDEEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL
 Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGQDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180
 LAFL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL
 Sbjct: 119 LAFLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 178

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLI 240
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 Sbjct: 179 VEAIESALESVNSPVESSPHQRPYTAADFIEGIYRTERDKGTYELTFKGDHKHEFQRLV 238

Query: 241 LFRPFSPIMKVKNEKLNMANLTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300
 LFRPF PIMKVK EKLN+ANTLINIVPLA+RVDKFR FMQNFREMCI+QDGRVHLTVVY
 Sbjct: 239 LFRPFGPIMKVKKEKLNLANLTLINIVPLARRVDKFRHFMQNFREMCIQDGRVHLTVVY 298

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360
 FGKEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD
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Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDVPPLEQQLVIKKETGFWRD 420
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 Sbjct: 359 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVPPPLGQQLVIKKETGFWRD 418

Query: 421 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLSNLIVVRTPVRLGFHLWHEKR 480
 FGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLSNLIVVRTPVRLGFHLWHEK
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Query: 481 CMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLR 521
 CMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLR
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☐ >gi|26324624|dbj|BAC26066.1| unnamed protein product [Mus musculus]
 Length = 530

Score = 1001 bits (2588), Expect = 0.0

Identities = 476/521 (91%), Positives = 496/521 (95%), Gaps = 4/521 (0%)

Query: 3 MVRRLGLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ 62
 MVRRLGL WISRVV+LLVLLCCAISVLYMLACTPKGDE+EQL LPRAN PTGK+GYQAVLQ
 Sbjct: 1 MVRRLGLGWISRVVILLVLLCCAISVLYMLACTPKGDEEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120
 E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL
 Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGQDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180
 LAFL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL
 Sbjct: 119 LAFLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 178

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLI 240
 VEAIESA+E+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTYELTFKGDHKHEF+RL+
 Sbjct: 179 VEAIESAMESLNSPVESSPHQRPYTAADFIEGIYRTERDKGTYELTFKGDHKHEFQRLV 238

Query: 241 LFRPFSPIMKVKNEKLNMANLTLINIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300
 LFRPF PIMKVK EKLN+ANTLINIVPLA+RVDKFR FMQNFREMCI+QDGRVHLTVVY
 Sbjct: 239 LFRPFGPIMKVKKEKLNLANLTLINIVPLARRVDKFRHFMQNFREMCIQDGRVHLTVVY 298

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360
 FGKEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD
 Sbjct: 299 FGKEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 358

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG+IYGHHDVAPP LQQQLVIKKETGFWRD
 Sbjct: 359 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVAPP LQQQLVIKKETGFWRD 418

Query: 421 FGFGMTCQYRSDFINIGGFDDLKIGWGGEDVHLYRKYLHSNLIVVRTPV RGLFHLWHEKR 480
 FGFGMTCQYRSDFINIGGFDDLKIGWGGEDVHLYRKYLHSNLIVVRTPV RGLFHLWHEK
 Sbjct: 419 FGFGMTCQYRSDFINIGGFDDLKIGWGGEDVHLYRKYLHSNLIVVRTPV RGLFHLWHEKH 478

Query: 481 CMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLR 521
 CMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLR
 Sbjct: 479 CMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLR 519

☐ >gi|9651083|dbj|BAB03554.1| hypothetical protein [Macaca fascicularis]
 Length = 453

Score = 915 bits (2364), Expect = 0.0
 Identities = 443/453 (97%), Positives = 448/453 (98%)

Query: 1 MMMVRRGLLAWISRNVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAV 60
 MMMVRRGLLAWISRNVVLLVLLCCAISVLYMLACTPKGD+EQLALPRANSPTGKEGYQA+
 Sbjct: 1 MMMVRRGLLAWISRNVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAI 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120
 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLG DRSPPEKTQADL
 Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGPDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL 180
 LAFLHSQVDKAEV+AGVKL TEYAAVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL
 Sbjct: 121 LAFLHSQVDKAEVHAGVKLTTEYAAVPFDSFTLQKVYQLETGLTRHPEEKPV RKDKRDEL 180

Query: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240
 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRL+
 Sbjct: 181 VEAIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLV 240

Query: 241 LFRPFSPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY 300
 LFRPF PI+KVK EKLNMANTLINVIVPLAKRVDKF QFMQNFREMCIEQDGRVHLTVVY
 Sbjct: 241 LFRPFGPIIKVKEKELNMANTLINVIVPLAKRVDKFWQFMQNFREMCIEQDGRVHLTVVY 300

Query: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360
 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD
 Sbjct: 301 FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVD 360

Query: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420
 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD
 Sbjct: 361 IYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIIYGHHDVAPPLEQQQLVIKKETGFWRD 420

Query: 421 FGFGMTCQYRSDFINIGGFDDLKIGWGGEDVHL 453
 FGFGMTCQYRSDFINIGGFDDLKIGWGGEDVHL
 Sbjct: 421 FGFGMTCQYRSDFINIGGFDDLKIGWGGEDVHL 453

☐ >gi|34877724|ref|XP_224757.2| similar to chondroitin beta1,4 N-acetylgalactosa
 [Rattus norvegicus]
 Length = 617

Score = 828 bits (2139), Expect = 0.0
 Identities = 395/448 (88%), Positives = 417/448 (93%)

Query: 3 MVRRLGLLAWISRNVVLLVLLCCAISVLYMLACTPKGDDEQLALPRANSPTGKEGYQAVLQ 62
 MVRRLGL+ WISRNV+LLVLLCCAISVLYMLACTPKGD+EQL LPRAN PTGK+GYQAVLQ
 Sbjct: 1 MVRRLGLVGWISRNVILLVLLCCAISVLYMLACTPKGDQEQLGLPRANGPTGKDG YQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLA 122
E EEQHRNYV+SLKRQIAQLK+ELQ RSEQLR+GQ QASDA L P K QAD+LA
Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQLRSGQDQASDATSLRSGWDPEPKAQADILA 120

Query: 123 FLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVE 182
FL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVE
Sbjct: 121 FLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDELVE 180

Query: 183 AIESALETLNPAENSPNHRPYTASDFIEGIYRTERDKGTYELTFKGDHKHEFKRLILF 242
AIESALE+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTYELTFKGDHKHEF+RL+LF
Sbjct: 181 AIESALESLSNPVLESSPHQRPYTAADFIEGIYRTERDKGTYELTFKGDHKHEFQRLVLF 240

Query: 243 RPFSPIMKVKNEKLNMAANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFG 302
RPF PIMKVK EKLNMANTLINIVIVPLA+RVDKFR FMQNFREMCI+QDGRVHLTVVYFG
Sbjct: 241 RPFGPIMKVKKEKLNMAANTLINIVIVPLARRVDKFRHFMQNFREMCIQDGRVHLTVVYFG 300

Query: 303 KEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIY 362
KEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNV+LFFCDVDIY
Sbjct: 301 KEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIY 360


Query: 363 FTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFG 422
FTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDV LEQQLVIKKETGFWRDFG
Sbjct: 361 FTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDVPALEQQLVIKKETGFWRDFG 420

Query: 423 FGMTQCYSRSDFINIGGFDLDIKGWGGED 450
FGMTQCYSRSDFINIG F + + GED
Sbjct: 421 FGMTQCYSRSDFINIGVFLVTLTDLMQGED 448

Score = 201 bits (510), Expect = 5e-50
Identities = 90/97 (92%), Positives = 93/97 (95%)

Query: 436 IGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVVRGLFHLWHEKRCMDELTPEQYKCMQ 495
+ GFDLDIKGWGGEDVHLYRKYLHSNLIV+RTPVRGLFHLWHEK CMDDELTPEQY+MCMQ
Sbjct: 521 VRGFDLDIKGWGGEDVHLYRKYLHSNLIVIRTVPVRGLFHLWHEKHCMDELTPEQYRMCMQ 580

Query: 496 SKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT 532
SKAMNEASHGQLGMLVFRHEIEAHLRKQK K SSKKT
Sbjct: 581 SKAMNEASHGQLGMLVFRHEIEAHLRKQKLKASSKKT 617

 >gi|47219910|emb|CAF97180.1| unnamed protein product [Tetraodon nigroviridis]
Length = 607

Score = 720 bits (1858), Expect = 0.0
Identities = 368/609 (60%), Positives = 447/609 (73%), Gaps = 83/609 (13%)

Query: 3 MVRRGLLAWISRVVLLVLLCCAISVLYMLACTP-KGDEEQLA--LPRA----- 48
M+RRGLLAW+SRV +LVLLC ++S+LY++ C+P D L LPRA
Sbjct: 1 MLRRGLLAWVSRVGGVLVLLCSSLSLLYLMTCSPPHSDNHPLGHVLPRAAPVRPSLGGTG 60

Query: 49 --NSPTGK-----EGYQAVLQEWEQHRNYVSSLKRQIAQLKEELQERSEQLR 94
+ T K + YQ +LQE EEQHR ++SSLK+QIAQLKE LQERS+QL+
Sbjct: 61 AGDVGTAARAAQNGAAPPQSYQVLLQEREEQHRLHISSLKQQAQLKEALQERSQQLK 120

Query: 95 NGQYQASDAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQ 154
Q S GLG + P+ QADL +L SQ+ KAEV AG +L +EYA VPF+SFTLQ
Sbjct: 121 G--VQESIKTGLG-EAHGPKSQQADLDQDYLRSQLTKAEVTAGTRLPSEYAVVPFESFTLQ 177

Query: 155 KVYQLETGLTRHPPEKPVRKDKRDELVEAIESALETLN-----NPAENSPNHRPYT 205
+VYQLETGLTRHPPEKPVRKD+RDEL E +E+AL +LN PA+ +P + Y+
Sbjct: 178 RVYQLETGLTRHPPEKPVRKDRDELGEVLETALHSLNAPSAAQDDKTPAQKAPTSKVYS 237

Query: 206 ASDFIE-----GIYRTERDKGTYELTFKGDHKHEFKRLILFRPFSPIMKV 251
SDF+E GI RTE+DKGT+YEL F+G+ +EF+RL+LFRPF P+MKV
Sbjct: 238 PSDFVEDSSLSSVVHPGAFSGISRTEKDKGTYELIFRGEAANEFRRLVLFRRPFGPLMKV 297

Query: 252 KNEKLNMAANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKG 311
 ++E+++ A+ IN++VPL++R DKF+QFM NFRE+C+ QDGRVHLTVVYFGKE+++EV+
 Sbjct: 298 RSERVAASIPINIVVPLSRRSDKFKQFMHNFREVCVRQDGRVHLTVVYFGKEQMSEVRS 357

Query: 312 ILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTC 371
 LENTS+ F+N+T +QL+ EFSRG+GLDVGAR W+G NVLLFFCDVDIYFT++FLN C
 Sbjct: 358 TLENTSREVRFKNYTLLQLDEEFSRGRGLDVGARAWRGGNVLLFFCDVDIYFTADFLNAC 417

Query: 372 RLNTQPG-----KKVFYPVLF SQYNPGIIGHHDAV 402
 RLN QPG KKVFYPVLF SQYNP +IYG + V
 Sbjct: 418 RLNAQPGETHHTHTLTCLVLLSLPGLMGSLSLPKKVFYPVLF SQYNPALIYGSSEHV 477

Query: 403 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNL 462
 PP+EQQLVIKK+TGFWRDFGFGMTCQYRSDFINIGGFD+DIKGWGGEDVHLYRKYLHSNL
 Sbjct: 478 PPVEQQQLVIKKDTGFWRDFGFGMTCQYRSDFINIGGFDIDIKGWGGEDVHLYRKYLHSNL 537

Query: 463 IVVRTPVRLGFLHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLRK 522
 +VVRTP RGLFHLWHEK C DEL P+QY+MCMQSKAMNEASHGQLGML FRHEIEAHLRK
 Sbjct: 538 LVVRTPARGLFHLWHEKHCADLPDQYRMCMQSKAMNEASHGQLGMLFFRHEIEAHLRK 597

Query: 523 QKQKTSSKK 531
 QKQ+ ++ K
 Sbjct: 598 QKQQNANLK 606

☐ >gi|24429592|ref|NP_061060.3| chondroitin beta1,4 N-acetylgalactosaminyltransf
 sapiens]
 gi|20988438|gb|AAH30268.1| Chondroitin beta1,4 N-acetylgalactosaminyltransferase
 sapiens]
 gi|27922994|dbj|BAC55935.1| beta-1,4-N-acethylgalactosaminyltransferase [Homo sa
 gi|27923015|dbj|BAC55936.1| chondroitin beta1,4 N-acetylgalactosaminyltransferase
 sapiens]
 Length = 542

Score = 665 bits (1717), Expect = 0.0

Identities = 316/512 (61%), Positives = 396/512 (77%), Gaps = 11/512 (2%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNVSSSLKRQIAQLKEELQE 88
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQE
 Sbjct: 29 MYLLECAPQTDGNASLPGVVGENYGYKEYYQALLQEEHYQTRATSLKRQIAQLKQELQE 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVP 147
 SE++R+ Q + + A G+G +S E+ +DLL FLHSQ+DKAEV+ G KL +EY +P
 Sbjct: 89 MSEKMRSIQERRNVGANGIGY-QSNKEQAPSDLLEFLHSQIDKAEVSIGAKLPSEYGVIP 147

Query: 148 FDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETNNPAENSPNHRP---- 203
 F+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ LE +NNP E+
 Sbjct: 148 FESFTLMKVQLEMGLTRHPEEKPVKDKRDELVEIEAGLEVINNPDDEDEQEDEEGPL 207

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLN 258
 + +DF+EG YRTERDKGT YEL FK E++ + LFRPF P+MKVK+E +++
 Sbjct: 208 GEKLIFNENDFVEGYRTERDKGTQYELFFKKADLTEYRHVTLFRPFGPLMKVKSEMIDI 267

Query: 259 ANT LINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSK 318
 ++IN+IVPLA+R + F QFMQNF++CI QD ++HLTVVYFGKE +++VK ILE+ +
 Sbjct: 268 TRSIINIIVPLAERTEAFVQFMQNF RDVCIHQDKKIHLTVVYFGKEGLSKVKSILESPTS 327

Query: 319 AANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG 378
 +NF N+T + LN EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN+PG
 Sbjct: 328 ESNFHNITLVSLNEEFNRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAEPG 387

Query: 379 KKVFPVLF SQYNPGIIGHHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGG 438
 KKVFPV+FS YNP I+Y + + PP+EQQLV KK++GFWRDFGFGMTCQYRSDF+ IGG
 Sbjct: 388 KKVFPVVFSLYNPAIVYANQEVPPPEQQQLVHKKDSGFWRDFGFGMTCQYRSDFLTIGG 447

Query: 439 FDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKCMQSKA 498
 FD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEKRC DELTPEQY+MC+QSKA
 Sbjct: 448 FDMEVKGWGGEDVHLYRKYLHGDLLIVIRTPVPGLFHLWHEKRCDELTPEQYRMCIQSKA 507

Query: 499 MNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
 MNEASH LGMLVFR EIE HL KQ +T+S+
 Sbjct: 508 MNEASHSHLGMLVFREEIETHLHKQAYRTNSE 539

>gi|31560032|ref|NP_084441.3| chondroitin sulfate GalNAcT-2 [Mus musculus]
 gi|26389329|dbj|BAC25717.1| unnamed protein product [Mus musculus]
 Length = 542

Score = 659 bits (1701), Expect = 0.0
 Identities = 315/514 (61%), Positives = 394/514 (76%), Gaps = 15/514 (2%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNVSSSLKRQIAQLKEELQE 88
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQ+
 Sbjct: 29 MYLLECAPQTDGNASLPGVVRENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQD 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAA 145
 SE++R Q + A G+G P + QA DLL FLHSQ+D+AEV+ G KL +EY
 Sbjct: 89 MSEKMRALQERKKLGANGVG---PGNREQAPSDLLEFLHSQIDRAEVSVAKLPSSEYGV 145

Query: 146 VPFDSFTLQKVYQLETGLTRHPPEKPVKDKRDELVEAIESALETNNPAENSPNHRP-- 203
 VPF+SFTL KV+QLE GLTRHPPEKPVKDKRDELVE IE+ +E +NNP E+
 Sbjct: 146 VPFESFTLMKVQLEMGLTRHPPEKPVKDKRDELVEIEAGVEVINNPDEDDAQEDEEG 205

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKL 256
 + +DFIEG YRTERDKGT YEL FK E++ + LFRPF P+MKVKNE +
 Sbjct: 206 PLGEKLIFNENDFIEGYRTERDKGTQYELFFKKADLMEYRHVTLFRPFGPLMKVKNELI 265

Query: 257 NMANTLINIVVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENT 316
 ++ ++IN+IVPLA+R + F QFMQNF++CI QD R+HLTVVYFGKE +++VK ILE+
 Sbjct: 266 DITRSVINIIVPLAERTEAFSQFMQNFQDVCIHQDKRIHLTVVYFGKEGLSKVKSILESV 325

Query: 317 SKAANFRNFTFIQLNGEFSRGGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTRCRLNTQ 376
 S ++F N+T + L+ EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +
 Sbjct: 326 SSESDFHNYTLVSLDEEFNRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAE 385

Query: 377 PGKKVFYFVLFYQYNPGIIYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINI 436
 PGKKVFYFV+FS YNP I+Y + D PP+EQQLV KK++GFWRDFGFGMTCQY+SDF+++
 Sbjct: 386 PGKKVFYFVVFSLYNPAIVYANQDVPVPPVEQQLVHKKDSGFWRDFGFGMTCQYQSDFLSV 445

Query: 437 GGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKCMQSKA 496
 GGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEK C DELTPEQY+MC+QS
 Sbjct: 446 GGFDMEVKGWGGEDVHLYRKYLHGDLLIVIRTPVPGLFHLWHEKHCDELTPEQYRMCIQS 505

Query: 497 KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
 KAMNEASH LGM+VFR EIE HLRKQ +T+S+
 Sbjct: 506 KAMNEASHSHLGMMVFREEIEMHLRKQAYRTNSE 539

>gi|26386533|dbj|BAB31761.2| unnamed protein product [Mus musculus]
 Length = 542

Score = 657 bits (1696), Expect = 0.0
 Identities = 314/514 (61%), Positives = 394/514 (76%), Gaps = 15/514 (2%)

Query: 29 LYMLACTPKGDEEQALPRANSPTGKEGYQAVLQEWEEQHRNVSSSLKRQIAQLKEELQE 88
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQ+
 Sbjct: 29 MYLLECAPQTDGNASLPGVVRENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQD 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAA 145
 SE++R Q + A G+G P + QA DLL FLHSQ+D+AEV+ G KL +EY
 Sbjct: 89 MSEKMRALQERKKLGANGVG---PGNREQAPSDLLEFLHSQIDRAEVSVAKLPSSEYGV 145

Query: 146 VPFDSTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRP-- 203
 VPF+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ +E +NNP E+
 Sbjct: 146 VPFEFTLMKVQFQLEMGLTRHPEEKPVKDKRDELVEIEAGVEVINNPDEDDAQEDEEG 205

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKL 256
 + +DFIEG YRTERDKGT YEL FK E++ + LFRPF P+MKVKNE +
 Sbjct: 206 PLGEKLIFNENDFIEGYRTERDKGTQYELFFKKADLMEYRHVTLFRPFGPLMKVKNELI 265


Query: 257 NMANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENT 316
 ++ ++IN+IVPLA+R + F QFMQNF++CI QD R+HLTVVYFGKE +++VK ILE+
 Sbjct: 266 DITRSVINIIVPLAERTEAFSQFMQNFQDVCIHQDKRIHLTVVYFGKEGLSKVKSILESV 325

Query: 317 SKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQ 376
 S ++F N+T + L+ EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +
 Sbjct: 326 SSESDFHNYTLVSLDEEFNRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAE 385

Query: 377 PGKKVFYFVLFQSYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINI 436
 PGKKVFYFV+F+ YNP I+Y + D PP+EQQLV KK++GFWRDFGFGMTCQY+SDF+++
 Sbjct: 386 PGKKVFYFVFNLYNPAIVYANQDVPPVEQQLVHKKDSGFWRDFGFGMTCQYQSDFLSV 445

Query: 437 GGFDLDIKGWGGEDVHLYRKYLHNSLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMS 496
 GGF+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEK C DELTPEQY+MC+QS
 Sbjct: 446 GGFDMEVKGWGGEDVHLYRKYLHGDLLIVRTVPVGLFHLWHEKHCADELTPEQYRMCIQS 505

Query: 497 KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSK 530
 KAMNEASH LGM+VFR EIE HLRKQ +T+S+
 Sbjct: 506 KAMNEASHSLGMMVFREEIEMHLRKQAYRTNSE 539

 >qi|47227595|emb|CAG09592.1|... unnamed protein product [Tetraodon nigroviridis]
 Length = 496

Score = 577 bits (1487), Expect = e-163

Identities = 284/494 (57%), Positives = 370/494 (74%), Gaps = 28/494 (5%)

Query: 52 TGKEGYQAVLQEWEEQHRNYVSSLRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLD 109
 T +EGY A+LQE E+ HR Y++SL RQI QLKE L ER++QL++ +A L GL+
 Sbjct: 3 TSREGYMALLQEREDSHRRYINSLTRQIQQLKEALLERTQQLQDSLEKAQTGGILPGGLE 62

Query: 110 RSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSTLQK----- 155
 TQ+DL FL SQ+D+AEVN+GVKL+ EY +P+D+FTLQ+
 Sbjct: 63 SLRKTPTQSDLKEFLRSQLDRAEVNSGVKLSGEYEVIPYDTFTLQRWVTELKPKSPMWLH 122

Query: 156 -----VYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAEN---SPNHRPY 204
 VYQLETGL+RHPEE+PVR+D+R EL A+E+AL LN P ++ + +
 Sbjct: 123 REALSPRVYQLETGLSRHPEERPVRDRRAELTGAVETALHLLNGPEQHGDGAAGKHTH 182

Query: 205 TASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAANTLIN 264
 + +DF+EG+ RTERD+GT+YELTFK +L+LFRPF P++KV++E +++++ L+N
 Sbjct: 183 SPADFVEGLTRTERDRGTVYELTFKDKGPRGLSQLVLFRPFGPLLKVRSESVDLSSVLVN 242

Query: 265 VIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRN 324
 V+VPL+ R + FR+F+ NFR CI+QDGRVHLTVV+FG + + +VK +L+ TS+ FRN
 Sbjct: 243 VVVPLSGRTEAFRRFIANFRACIQDGRVHLTVVHFGGDPVEQVKALLDQTSRETRFRN 302

Query: 325 FTFIQLNGEFSRGKGLDVGARFWKGS-NVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVY 383
 FT IQLN FSRG+GL++GAR W+ S NVLLFFCDVD++FT++FL +CRLN PGKKV+Y
 Sbjct: 303 FTLIQLNEVFSRGRGLEIGARAWRRSQNVLLFFCDVDVHFTADFLTSCRLNALPGKKVYY 362

Query: 384 PVLFSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDI 443
 PVLFS YNP +IY +H P L+QQLVI+KE+GFWRDFGFGMTCQYRSDFINIGGF I
 Sbjct: 363 PVLFSLYNPSVIYHNHTHPPSLQQLVIRKESGFWRDFGFGMTCQYRSDFINIGGFDRAI 422

Query: 444 KGWGGEDVHLYRKYLHNSLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMSKAMNEAS 503
 +GWG EDVHLYRKYLH L+VVR+P R LFHLWHEK C DEL P++Y+MCMQ+KA++EAS
 Sbjct: 423 RGWGLEDVHLYRKYLHSLKLMVVRSPSRSLFHLWHEKVCADLPDPKYRMCMQTKAVSEAS 482

Query: 504 HGQLGMLVFRHEIE 517
HG+LG LVFR E
Sbjct: 483 HGRLGELVFRRRDE 496

☐ >gi|38174240|gb|AAH60772.1| ChGn protein [Homo sapiens]
Length = 297

Score = 557 bits (1436), Expect = e-157
Identities = 282/284 (99%), Positives = 283/284 (99%)

Query: 1 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAV 60
MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAV
Sbjct: 1 MMMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAV 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120
LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL
Sbjct: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADL 120

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180
LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL
Sbjct: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180

Query: 181 VEAIESALETLNPNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240
VEAIESALETLNPNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI
Sbjct: 181 VEAIESALETLNPNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240

Query: 241 LFRPFSPIMKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFR 284
LFRPF PIMKV+NEKLNMAANTLINVIVPLAKRVDKFRQFMQNFR
Sbjct: 241 LFRPFGPIMKVENEKLNMAANTLINVIVPLAKRVDKFRQFMQNFR 284

☐ >gi|26340498|dbj|BAC33912.1| unnamed protein product [Mus musculus]
Length = 300

Score = 532 bits (1370), Expect = e-150
Identities = 262/302 (86%), Positives = 279/302 (92%), Gaps = 4/302 (1%)

Query: 3 MVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALPRANSPTGKEGYQAVLQ 62
MVRRGLL WISRVV+LLVLLCCAISVLYMLACTPKGDE+EQL LPRAN PTGK+GYQAVLQ
Sbjct: 1 MVRRGLLGWISRVVILLVLLCCAISVLYMLACTPKGDEEQLGLPRANGPTGKDGQAVLQ 60

Query: 63 EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGL--GLDRSPPEKTQADL 120
E EEQHRNYV+SLKRQIAQLK+ELQ RSEQ R+GQ QASDA L G DR P K QADL
Sbjct: 61 EREEQHRNYVNSLKRQIAQLKDELQARSEQFRSGQDQASDATSLRSGWDREP--KAQADL 118

Query: 121 LAFLHSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 180
LAFL QVDKAEV+AGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL
Sbjct: 119 LAFLRGQVDKAEVHAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPPEKPVRKDKRDEL 178

Query: 181 VEAIESALETLNPNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLI 240
VEAIESALE+LN+P E+SP+ RPYTA+DFIEGIYRTERDKGTLYELTFKGDHKHEF+RL+
Sbjct: 179 VEAIESALESINSPVESSPHQRPYTAADFIEGIYRTERDKGTLYELTFKGDHKHEFQRLV 238

Query: 241 LFRPFSPIMKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFRFREMCIQDGRVHLTVVY 300
LFRPF PIMKVK EKLN+ANTLINVIVPLA+RVDKFR FMQNFRFREMCI+QDGRVHLTVVY
Sbjct: 239 LFRPFGPIMKVKKEKLNLANANTLINVIVPLARRVDKFRHFMQNFRFREMCIQDGRVHLTVVY 298

Query: 301 FG 302
FG
Sbjct: 299 FG 300

☐ >gi|7023813|dbj|BAA92093.1| unnamed protein product [Homo sapiens]
Length = 275

Score = 523 bits (1347), Expect = e-147


Identities = 238/239 (99%), Positives = 239/239 (100%)

Query: 283 FREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDV 342
 FREMCIEQDGRVHLTVVYFGKEEINEVKG+LENTSKAANFRNFTFIQLNGEFSRGKGLDV
 Sbjct: 26 FREMCIEQDGRVHLTVVYFGKEEINEVKGVLENTSKAANFRNFTFIQLNGEFSRGKGLDV 85

Query: 343 GARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDV 402
 GARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDV
 Sbjct: 86 GARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDV 145

Query: 403 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNL 462
 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNL
 Sbjct: 146 PPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNL 205

Query: 463 IVVRTPVRLGFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521
 IVVRTPVRLGFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR
 Sbjct: 206 IVVRTPVRLGFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 264

 >gi|20072996|gb|AAH26599.1| 4732435N03Rik protein [Mus musculus]
 Length = 239


Score = 494 bits (1272), Expect = e-138
 Identities = 224/228 (98%), Positives = 226/228 (99%)

Query: 294 VHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVL 353
 VHLTVVYFGKEE+NEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVL
 Sbjct: 1 VHLTVVYFGKEEMNEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVL 60

Query: 354 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYGHHDVPPLEQQQLVIKK 413
 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG+IYGHHDVPPLEQQQLVIKK
 Sbjct: 61 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGVIYGHHDVPPLEQQQLVIKK 120

Query: 414 ETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGF 473
 ETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGF
 Sbjct: 121 ETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGF 180

Query: 474 HLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 521
 HLWHEK CDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR
 Sbjct: 181 HLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLR 228

 >gi|34858369|ref|XP_232316.2| similar to chondroitin betal,4 N-acetylgalactosa
 [Rattus norvegicus]
 Length = 462

Score = 486 bits (1251), Expect = e-136
 Identities = 214/317 (67%), Positives = 266/317 (83%)

Query: 214 YRTERDKGTYELTFKGDHKHEFKRLILFRPFSPIMKVKNEKLNMAANTLINVIVPLAKRV 273
 YRTERDKGT YEL FK E++ + LFRPF P+MKVK+E +++ ++IN+IVPLA+R
 Sbjct: 143 YRTERDKGTHYELFFKADLMERYHVTLFRPFGPLMKVKSELIDITRSVINIIVPLAERT 202

Query: 274 DKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGE 333
 + F QFMQNF++CI QD R+HLTVVYFGKE ++ VK ILE+ S +NF N+T + LN E
 Sbjct: 203 EAFSQFMQNFQDVCIHQDKRIHLTVVYFGKEGLSTVKSILESVSSESNFHNYTLVSLNEE 262

Query: 334 FSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPG 393
 F+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +PGKKVFYPV+FS YNP
 Sbjct: 263 FNRGRGLNVGARTWDKGEVLMFFCDVDIYFSAEFLNSCRLNAEPGKKVFYPVVFSLYNPA 322

Query: 394 IYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDIKGWGGEDVHL 453
 I+Y + + PP+EQQLV KK++GFWRDFGFGMTCQY+SDF+++GGFD+++KGWGGEDVHL
 Sbjct: 323 IVYANQEVPPPVEQQQLVHKKDSGFWRDFGFGMTCQYQSDFLSVGGFDMEVKGWGGEDVHL 382

Query: 454 YRKYLHSNLIVVRTPVRLGFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLGMLVFR 513
 YRKYLH +LIV+RTPV GLFHLWHEK C DELTPQY+MC+QSKAMNEASH LGM+VFR

Sbjct: 383 YRKYLHGDIVIRTPVPGFLHLWHEKHCADLTPEQYRMCIQSKAMNEASHSHLGMMVFR 442

Query: 514 HEIEAHLRKQKQKTSSK 530

EIE HLRKQ +T+S+

Sbjct: 443 EEIEMHLRKQAYRTNSE 459

Score = 99.8 bits (247), Expect = 2e-19

Identities = 63/144 (43%), Positives = 87/144 (60%), Gaps = 4/144 (2%)

Query: 3 MVRRG--LLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAV 60

M RRG L + +V L LL + +Y+L C P+ D GKE YQA+

Sbjct: 1 MSRRGPILHSRTQWLLVGLALLFSLVLFMYLLECAPQTDGNASLPGVVRENYGKEYYQAL 60

Query: 61 LQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQAS-DAAGLGLDRSPPEKTQAD 119

LQE EE ++ +SLKRQIAQLK+ELQ+ SE++R Q + A G+G + E+T +D

Sbjct: 61 LQEQEEHYQTRATSLKRQIAQLKQELQDMSEKMRALQERKKLGANGIGY-QGNREQTPSD 119

Query: 120 LLAFLLHSQVDKAEVNAGVKLATEY 143

LL FLHSQ+D+AEV+ G KL + Y

Sbjct: 120 LLEFLHSQIDRAEVSIGAKLPSYY 143

☐ >gi|47216537|emb|CAG04715.1| unnamed protein product [Tetraodon nigroviridis]
Length = 522

Score = 485 bits (1248), Expect = e-135

Identities = 235/413 (56%), Positives = 298/413 (72%), Gaps = 8/413 (1%)

Query: 34 CTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQL 93

CTP D + A GKE YQA+LQE EE+H N +SLKRQIAQLK+ELQE S++L

Sbjct: 34 CTPPADISLVLPGLAGENNGKEYYQALLQEQEERHLNRATSLKRQIAQLKQELQEMSDKL 93

Query: 94 RNGQYQASDAAGLGLDRSPPEKTQADLLAFLLHSQVDKAEVNAGVKLATEYAAVPFDSFTL 153

+ Q + A GL + ++ DLL +LHSQ+DKAEVN G + +EYA +PF+SFT

Sbjct: 94 KLLQDKKEPPAVQGLAETK-DQEPGDLDDLHLSQIDKAEVNTGARFPSEYALIPFESFTS 152

Query: 154 QKVYQLETGLTRHPPEEKPVRRDKRDELVEAIESALETNNP-----AENSPNHR-PYTA 206

KVYQLE GLTRHPPEEKPVRR+D+RDELVE +E+AL+ +NNP E+ P R YT

Sbjct: 153 SKVYQLEMGLTRHPPEEKPVRRDRRDELVEVVEAALDIINNPDDEEDGVEEDVPMQRQTYTE 212

Query: 207 SDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVI 266

F EG+YRTERDKGTLYEL F + F+ + LFRPF P+MKV++ + + +IN+I

Sbjct: 213 VHFTEGLYRTERDKGTLYELFFAKEDSSSRHVTLFRPFGPLMKVRSTSVETSGAIINII 272

Query: 267 VPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFT 326

VPL+ RV+ F QF+ NFRE+CI D RVHLTVVYFG+E + EVK LE S+ +F N+T

Sbjct: 273 VPLSGRVEAFSQFLHNFREVCILHDDRVLTVVYFGQEGLEVKSSLEKVSREESFSNYT 332

Query: 327 FIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVL 386

I ++ EFSRG+GLD+GA WK +VL+FFCDVDI+F+ EFLNTCRL+ P K+VFYPV+

Sbjct: 333 LIPVDEEFSRGRGLDIGAHAWKRGDVLMMFFCDVDIHFSLEFLNTCRLHAAPNKRVPV 392

Query: 387 FSQYNPGIYGHHDVPPLEQQLVIIKKTGFWRDFGFGMTCQYRSDFINIGGF 439

FS YNP I+YG+ + PP+E QL+ KK+ GFWRDFGFGMTCQYRSDF+NI F

Sbjct: 393 FSLYNPAIVYGNLELAPPIELQLIHKKDAGFWRDFGFGMTCQYRSDFLNIAF 445

☐ >gi|31198419|ref|XP_308157.1| ENSANGP00000021559 [Anopheles gambiae]
gi|21292063|gb|EAA04208.1| ENSANGP00000021559 [Anopheles gambiae str. PEST]
Length = 648

Score = 382 bits (982), Expect = e-105

Identities = 222/547 (40%), Positives = 310/547 (56%), Gaps = 68/547 (12%)

Query: 47 RANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQA----- 100

+A++ + GY +LQ+ EE++ V+ L +I LK ++ QL+NG A

Sbjct: 81 QADAEQQQNGYMQMLQQREEENLKEVAKLTAEIKALKLQIL---QLKNGLTNAGMGMVQ 136

Query: 101 ----SDAAGLGLDRSP-----PEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAAVPFD 149
A L D S P+ +Q D AF+ QV AE+ G+ L EY +PF+

Sbjct: 137 PNVVEAAVSLSDSSAIVANAPQTSQMLHDCATFIRRQVGSAEILHGLPLNNEYELIPFN 196

Query: 150 SFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRPYTASDF 209
FT +VY +E GL + EKP+ KR +++ A+ ALETLN A +S YT DF

Sbjct: 197 HFTFSRVYPIELGLGKRVVEKPIGY-KRKDILSALNKALETNLNRNASSSAQR--YTLDDF 253

Query: 210 IEGIYRTERDKGTLYELTFKGDHK-----HEFKRLILFRPFSPIMKVKN 253
IEGIYR E GT YEL F+ H +LI+ RPF+ + V+

Sbjct: 254 IEGIYRNEPTTGTQYELYFRTKESANRSQQQQQIAQHSHSGTTKLIVMRPFASLQTVQL 313

Query: 254 EKLN--MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVKG 311
E + +I +I+PL+ R F+ FM+ + ++ ++ D RVHLTVVYFG+E + E +

Sbjct: 314 EAYSKHQEKEIIYIILPLSGRTSTFQSFMEKYVKIALKHDKRVHLTVVYFGEEGLAEART 373

Query: 312 ILENT---SKAANFRNFTFIQLNGEFSRGKGLDVGAR-FW----KGSNVLLFFCDVDI 361
I+ + A N + LN FSR K L VGA W K +++LLF CDVDI

Sbjct: 374 IMSRVIGMKNSGATNSNLKLLALNETFSRAKALRVGAENVWSSQADKNNDILLFMCDDVI 433

Query: 362 YFTSEFLNTCRLNTQPGKKVFYPVLFSSQYNPGIYG-HHDAVPPLEQQQLVIKKETGFWRD 420
F+++FL+ CR NT+P KKV+YPV+FS YNP ++Y VPP QLVI K++GFWRD

Sbjct: 434 VFSAKFLDRCRWNTKPNKKVYYPVVFSLYNPHVVYTLQGKDVPPETDQLVISKDSGFWRD 493

Query: 421 FGFGMTCQYRSDFINIGGFDLIDKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEKR 480
FG+GMTCQYRSDF+ + GFD +I GWGGEDV LYRKY+ S++ V+R G+FH+WH K

Sbjct: 494 FGFGMTCQYRSDFLRVGRGFDEEIIGWGGEDVMYLYRKYVRSIKVIRATDPGVFHIWHPKV 553

Query: 481 CM-----DELTPEQYKMCQSKAMNEASHGQLGMLVFRHEIEAHL-----RKQKQ 525
C LT +QY+ C++S+A+NEASH QLG L FR +I A+ K Q

Sbjct: 554 CTGPVMSVTSNQRLTLDQYRACIRSRALNEASHAQLGFLAFRDDIAANEYILAQGAQLNQ 613

Query: 526 KTSSKKT 532
++S+ KT

Sbjct: 614 ESSTTKT 620

☐ >gi|34365000|emb|CA546036.1| hypothetical protein [Homo sapiens]
Length = 216

Score = 361 bits (927), Expect = 2e-98
Identities = 154/211 (72%), Positives = 183/211 (86%)

Query: 320 ANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379
+NF N+T + LN EF+RG+GL+VGAR W VL+FFCDVDIYF++EFLN+CRLN +PGK

Sbjct: 3 SNFHNITLVSLNEEFNRRGRGLNVGARAWDKGEVLMFFCDVDIYFSAEFLNSCRLNAEPK 62

Query: 380 KVFYPVLFSSQYNPGIYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439
KVFYPV+FS YNP I+Y + + PP+EQQLV KK++GFWRDFGFGMTCQYRSDF+ IGGF

Sbjct: 63 KVFYPVVFSLYNPAIVYANQEVPPPVEQQLVHKKDSGFWRDFGFGMTCQYRSDFLTIGGF 122

Query: 440 DLDIKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEKRCMDLTPEQYKMCQSKAM 499
D+++KGWGGEDVHLYRKYLSH +LIV+RTPV GLFHLWHEKRC DELTPEQY+MC+QSKAM

Sbjct: 123 DMEVKGWGGEDVHLYRKYLSHGLDILVIRTPVSGLFHLWHEKRCADLTPEQYRMCIQSKAM 182

Query: 500 NEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
NEASH LGMLVFR EIE HL KQ +T+S+

Sbjct: 183 NEASHSHLGMLVFREIEIETHLHKQAYRTNSE 213

☐ >gi|24652379|ref|NP_610567.1| CG12913-PA [Drosophila melanogaster]
gi|7303771|gb|AAF58819.1| CG12913-PA [Drosophila melanogaster]
Length = 540

Score = 351 bits (901), Expect = 2e-95

Identities = 208/519 (40%), Positives = 293/519 (56%), Gaps = 59/519 (11%)

Query: 39 DEEQALPRANSPTGKEGYQAVLQEWEE---EQHRNVSSSLKRQIAQLKEELQERSEQLRN 95
 DE +AN+P+ G+ L E E E+ + V +L+ QI L+ + + N
 Sbjct: 34 DELTTRETQANNPSESSGFSYTLSEAEIERLKQEV LALRTQILFLQN--NRSTAKPSN 91

Query: 96 GQYQASDAAGLGLDRSPPEKT---QADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDSFT 152
 G Q + PP D +++ QV AE+ G+ L EY +P++ FT
 Sbjct: 92 GSLQLQETTA-----GPPTAPLGHYDCSSYIRKQVGAAEILHGLPLNNEYELIPYNHFT 146

Query: 153 LQKVYQLETGLTRHPEEKPVRRKDKRDELVEAIESALETINNPAENSPNHRP----- 203
 +VY ++ GL + EKP+ +RD L+EA+ ALE+LN +S R
 Sbjct: 147 FTRVYPIDLGLGKRVEKPIGYRRRD-LIEAVNKALESLNR--NHSARIRAKGAGSAAAY 203

Query: 204 -----YTASDFIEGIYRTERDKGTLYELTFKGDHKHE---FKRLILFRPFSPIMKVKNE 254
 YT DFIEGIYR E GT YEL F+ KH+ +R ++ RPF+P+ V+
 Sbjct: 204 ASDVIKYTLDDFIEGIYRNEPTTGTQYELYFQ-SVKHQASPVRRALVMRPFAPLQTVQLS 262


Query: 255 KLNMA-----NTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK 303
 +L+ + +I+VI+PLA R+ FR F+Q F ++ +D R+ L VVYFG
 Sbjct: 263 ELSSSVDNSGAPPSHSPPIIHVILPLAGRLHSFRGFLQMFAL---EDRRLELIVVYFG- 318

Query: 304 EEINEVGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGS--NVLLFFCDVDI 361
 G+ + S A + F+ LN FSR K L +GA + + +VLLF CDVDI
 Sbjct: 319 -----TSGLEQARSLAGRSQRTQFLALNETFSRAKALRLGAEHIQPAEEDVLLFMCDVDI 373

Query: 362 YFTSEFLNTCRLNTQPGKKVFPVLFVSQYNPGIYIG-HHDAVPPLEQQLVIKKETGFWRD 420
 FT++FL CR N PGKKV+YPV+FS YNP ++Y +P E+QLVI ++TGFWRD
 Sbjct: 374 MFTTKFLERCWNAAPGKKVYYPVVFSLYNPHVVYSLQGKPLPSEEEQLVISRDTGFWRD 433

Query: 421 FGFGMTCQYRSDFINIGGFDLD-IKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEK 479
 FG+GMTQCQYRS+F+ + GFD + I GWGGEDV LYRKY+ S + ++R G+FH WH K
 Sbjct: 434 FGYGMTQCQYRSNFLKVRGFDEEEIVGWGGEDVMLYRKYVRSKIKIIRATDPGIFHRWHTK 493

Query: 480 RCMDELTPQYKMCQMCKAMNEASHGQLGMLVFRHEIEA 518
 C LT +QY+ C++S+A+NEASH QLG L FR +I A
 Sbjct: 494 ICSSSLTADQYRACIRSRALNEASHAQLGFLAFRDDIAA 532

 >gi|11360289|pir||T46919 hypothetical protein DKFZp762L037.1 - human (fragment)
 gi|7018526|emb|CAE75673.1| hypothetical protein [Homo sapiens]
 Length = 152


Score = 317 bits (812), Expect = 5e-85

Identities = 141/141 (100%), Positives = 141/141 (100%)

Query: 381 VFYPVLFVSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFD 440
 VFYPVLFVSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFD
 Sbjct: 1 VFYPVLFVSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFD 60

Query: 441 LDIKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCQMCKAMN 500
 LDIKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCQMCKAMN
 Sbjct: 61 LDIKGWGGEDVHLYRKYLSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCQMCKAMN 120

Query: 501 EASHGQLGMLVFRHEIEAHLR 521
 EASHGQLGMLVFRHEIEAHLR
 Sbjct: 121 EASHGQLGMLVFRHEIEAHLR 141

 >gi|13677033|dbj|EAB35092.1| unnamed protein product [Homo sapiens]
 Length = 180

Score = 317 bits (811), Expect = 5e-85

Identities = 134/177 (75%), Positives = 158/177 (89%)

Query: 354 LFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFVSQYNPGIYGHHDVPPLEQQLVIKK 413
 +FFCDVDIYF++EFLN+CRLN +PGKKVFYPV+FS YNP I+Y + + PP+EQQLV KK


Sbjct: 1 MFFCDVDIYFSAEFLNSCRLNAEPGKKVFYPVVFSLYNPAIVYANQEVPPPVEQQLVHKK 60

Query: 414 ETGFWRDFGFGMTCQYRSDFINIGGFDLIKGWGGEDVHLYRKYLHSNLIVVRTPVRLGF 473
 ++GFWRDFGFGMTCQ+RSDF+ IGGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLF

Sbjct: 61 DSGFWRDFGFGMTCQHRSDFLTIGGFDMEVKGWGGEDVHLYRKYLHGDIVIRTPVPGLF 120

Query: 474 HLWHEKRCMDELTPPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
 HLWHEKRC DELTPPEQY+MC+QSKAMNEASH LGMLVFR EIE HL KQ +T+S+

Sbjct: 121 HLWHEKRCADELTPEQYRMCIQSKAMNEASHSHLGMLVFREEIETHLHKQAYRTNSE 177

 >gi|34365310|emb|CAE45982.1| hypothetical protein [Homo sapiens]
 Length = 333

Score = 314 bits (805), Expect = 3e-84

Identities = 163/303 (53%), Positives = 216/303 (71%), Gaps = 11/303 (3%)

Query: 29 LYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQE 88
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQE

Sbjct: 29 MYLLECAPQTDGNASLPGVVGENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQE 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVP 147
 SE++R+ Q + + A G+G +S E+ +DLL FLHSQ+DKAEV+ G KL +EY +P

Sbjct: 89 MSEKMRSLQERRNVGANGIGY-QSNKEQAPSDDLLEFLHSQIDKAEVSIGAKLPSEYGVIP 147

Query: 148 FDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRP---- 203
 F+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ LE +NNP E+

Sbjct: 148 FESFTLMKVFQLEMGLTRHPEEKPVKDKRDELVEIEAGLEVINNPDDEDEQEDEEGPL 207

Query: 204 -----YTASDFIEGIYRTERDKGTYELTFKGDHKEFKRLILFRPFSPIMKVKNELNM 258
 + +DF+EG YRTERDKGT YEL FK E++ + LFRPF P+MKVK+E +++

Sbjct: 208 GEKLIFNENDFVEGYRTERDKGTQYELFFKKADLTEYRHVTLFRPFGPLMKVKSEMDI 267

Query: 259 ANTLINIVIVPLAKRVDKFRQFMQNFRMCIEQDGRVHLTVVYFGKEEINEVKGILENTSK 318
 ++IN+IVPLA+R + F QFMQNFR++CI QD ++HLTVVYFGKE +++VK ILE+ ++

Sbjct: 268 TRSIINIIVPLAERTEAFVQFMQNFRDVCIHQDKKIHLTVVYFGKEGLSKVKSILESVTR 327

Query: 319 AAN 321
 A+

Sbjct: 328 LAS 330

 >gi|37805317|gb|AAH60169.1| Galnact2 protein [Mus musculus]
 Length = 293

Score = 264 bits (675), Expect = 4e-69

Identities = 144/268 (53%), Positives = 182/268 (67%), Gaps = 15/268 (5%)

Query: 29 LYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQEWEEQHRNYVSSLKRQIAQLKEELQE 88
 +Y+L C P+ D GKE YQA+LQE EE ++ +SLKRQIAQLK+ELQ+

Sbjct: 29 MYLLECAPQTDGNASLPGVVRENYGKEYYQALLQEQQEHHYQTRATSLKRQIAQLKQELQD 88

Query: 89 RSEQLRNGQYQAS-DAAGLGLDRSPPEKTQA--DLLAFLHSQVDKAEVNAGVKLATEYAA 145
 SE++R Q + A G+G P + QA DLL FLHSQ+D+AEV+ G KL +EY

Sbjct: 89 MSEKMRALQERKKLGANGVGY---PGNREQAPSDLLLEFLHSQIDRAEVSIGAKLPSEYGV 145

Query: 146 VPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIESALETLNPAENSPNHRP-- 203
 VPF+SFTL KV+QLE GLTRHPEEKPVKDKRDELVE IE+ +E +NNP E+


Sbjct: 146 VPFESFTLMKVFQLEMGLTRHPEEKPVKDKRDELVEIEAGVEVINNPDEDDAQEDEEG 205

Query: 204 -----YTASDFIEGIYRTERDKGTYELTFKGDHKEFKRLILFRPFSPIMKVKNEL 256
 + +DFIEG YRTERDKGT YEL FK E++ + LFRPF P+MKVKNE +

Sbjct: 206 PLGEKLIFNENDFIEGYRTERDKGTQYELFFKKADLMEYRHVTLFRPFGPLMKVKNELI 265

Query: 257 NMANTLINIVIVPLAKRVDKFRQFMQNFR 284
 ++ ++IN+IVPLA+R + F QFMQNFR

Sbjct: 266 DITRSVINIIVPLAERTEAFSQFMQNFR 293

 >gi|47201472|emb|CAF87906.1| unnamed protein product [Tetraodon nigroviridis]
Length = 245

Score = 221 bits (563), Expect = 3e-56

Identities = 127/309 (41%), Positives = 167/309 (54%), Gaps = 71/309 (22%)

Query: 178 DELVEAIESALETNNP-----AENSPNHR-PYTASDFIEGIYRTERDKGTLYELTFKG 230
DELVE +E+AL+ +NNP E+ P R YT F EG+YRTERDKGTLYEL F
Sbjct: 1 DELVEVVEAALDIINNPDEEDGVEEDVPMQRQTYTEVHFTEGLYRTERDKGTLYELFFAK 60


Query: 231 DHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVDKFRQFMQNFREMCIEQ 290
+ F+ + LFRPF P+MKV++ + + +IN+IVPL+ RV+ F QF+ NFRE+CI
Sbjct: 61 EDSSSFHVTFLFRPFGLMKVRSVETSGAIINIIIVPLSGRVEAFSQFLHNFREVCILH 120

Query: 291 DGRVHLTVVYFGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGS 350
D RVHLTVVYFG+E + EVK LE S++ + ++ A FW+
Sbjct: 121 DRRVHLTVVYFGQEGLEVKSSLEKVSRSIHKD-----AGFWRD- 160

Query: 351 NVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYNPGIYGHHDVAPPLEQQLV 410
F + + S+FLN + + S +N +A+PPL
Sbjct: 161 ----FGFGMTCQYRSDFLNIGKRSRG-----LSLFNAEFTENGCEAIPPLA---- 202

Query: 411 IKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPVR 470
GGFDL++KGWG EDVHLYRKYL S+LIV+RTPV
Sbjct: 203 -----GGFDLEVKGWGEDVHLYRKYLRSIDLIVIRTPVS 236

Query: 471 GLFHLWHEK 479
LFHLWHEK
Sbjct: 237 SLFHLWHEK 245

 >gi|37573674|dbj|BAC98832.1| chondroitin sulfate synthase [Homo sapiens]
Length = 882

Score = 207 bits (527), Expect = 5e-52

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)


Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315
++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG
Sbjct: 621 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIILFSRDSGQDSSKHIELIKGYQNK 680

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTCRLN 374
KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N
Sbjct: 681 YPKA----EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCVDLIFREDFLQRCRDN 734

Query: 375 TQPGKKVFYPVLFSQYNPGIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI 434
T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +
Sbjct: 735 TIQQQQVYPIIFSQYDPKVTNGGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDL 791

Query: 435 NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPVRGLFHLWHEKRCMDELTPQYKMCM 494
GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+
Sbjct: 792 GAGGFDTSIQGWGLEDVDLYNKVILSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCL 851

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529
SKA AS QL L +E HL + +T S
Sbjct: 852 GSKASTFASTMQLAEL---WLEKHLGVRYNRTLS 882

 >gi|42657273|ref|XP_373440.2| chondroitin sulfate synthase 3 [Homo sapiens]
Length = 882

Score = 207 bits (527), Expect = 5e-52

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315
++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG

Sbjct: 621 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIIILFSRDSGQDSSKHIELIKGYQNK 680

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTCRLN 374
KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N

Sbjct: 681 YPKA----EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 734

Query: 375 TQP GKVFYFVPLFSQYNPGI IYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI 434
T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +

Sbjct: 735 TIQQQQVYYP IIFSQYDPKVTNGGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDLL 791


Query: 435 NIGGFDDL DIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTP EQYKMCM 494
GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+

Sbjct: 792 GAGGFDTSIQGWGLEVDLYNKVILSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCL 851

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529

SKA AS QL L +E HL + +T S

Sbjct: 852 GSKASTFASTMQLAEL----WLEKHLGVRYNRTLS 882

 >gi|41529141|emb|CAE17326.1| chondroitin synthase 2 [Homo sapiens]
Length = 882

Score = 207 bits (526), Expect = 6e-52

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315
++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG

Sbjct: 621 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVIIILFSRDSGQDSSKHIELIKGYQNK 680

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTCRLN 374
KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N

Sbjct: 681 YPKA----EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 734

Query: 375 TQP GKVFYFVPLFSQYNPGI IYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI 434
T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +

Sbjct: 735 TIQQQQVYYP IIFSQYDPKVTNGGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDLL 791


Query: 435 NIGGFDDL DIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTP EQYKMCM 494
GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+

Sbjct: 792 GAGGFDTSIQGWGLEVDLYNKVILSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCL 851

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529

SKA AS QL L +E HL + +T S

Sbjct: 852 GSKANTFASTMQLAEL----WLEKHLGVRYNRTLS 882

 >gi|27681143|ref|XP_225912.1| similar to carbohydrate (chondroitin) synthase 2
norvegicus]
Length = 561

Score = 206 bits (524), Expect = 1e-51

Identities = 112/271 (41%), Positives = 160/271 (59%), Gaps = 13/271 (4%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYF---GKEEINEVKGILENTSK 318
++++VPL R D F +FM+NF CI V L ++ F G+E I ++ I E ++

Sbjct: 300 VHILVPLVGRYDIFLRFMENFESTCIIPKQNVKLVIIILFSRDSGQESIKHIELIQEYQNR 359

Query: 319 AANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG 378
+ T I + GEFSRG GL++G+ + ++ LL FCDVD+ F +FL CR NT G

Sbjct: 360 YPS-AEMTLIPMKGEFSRGLGLEMGSSQFD-NDTLLLFCDVDLIFRGDFLQRCRDNTVQG 417

Query: 379 KKVYFVPLFSQYNPGI IYGHDAVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGG 438
++V+YP++FSQY+P + P E V KETGFWRD+G+G+TC Y+SD + GG

Sbjct: 418 QQVYYP IIFSQYDPKVTVMGNS---PTEGDFVFSKETGFWRDYGYGITCIYKSDLLGAGG 474

Query: 439 FDL DIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTP EQYKMCMQSKA 498
FD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+ SKA

Sbjct: 475 FDTSIQGWGLEDVDLYNKVIQSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCLGSKA 534

Query: 499 MNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529

AS +L L +E HL + +T S

Sbjct: 535 STFASTMKLAEL---WLEKHLGVRDNRTLS 561

☐ >gi|28411190|emb|CAD43233.1| chondroitin synthase 2 [Homo sapiens]
Length = 573

Score = 206 bits (523), Expect = 1e-51

Identities = 113/275 (41%), Positives = 160/275 (58%), Gaps = 21/275 (7%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKE-----EINEVKGILEN 315

++++VPL R D F +FM+NF MC+ V L ++ F ++ I +KG

Sbjct: 312 VHILVPLIGRYDIFLRFMENFENMCLIPKQNVKLVILFSRDSGQDSSKHIELIKGYQNK 371

Query: 316 TSKAANFRNFTFIQLNGEFSRGKGLDVG-ARFWKGSNVLLFFCDVDIYFTSEFLNTRCLN 374

KA T I + GEFSRG GL++ A+F ++ LL FCDVD+ F +FL CR N

Sbjct: 372 YPKA---EMTLIPMKGEFSRGLGLEMASAQF--DNDTLLLFCDVDLIFREDFLQRCRDN 425

Query: 375 TQPGKKVFYPVLFSSQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI 434

T G++V+YP++FSQY+P + G + PP + + K+TGFWRD+G+G+TC Y+SD +

Sbjct: 426 TIQGGQVYYPPIIFSQYDPKVTNGGN--PPTDDYFIFSKKTGFWRDYGYGITCIYKSDLL 482

Query: 435 NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPVRGLFHLWHEKRCMDELTPQYKMCM 494

GGFD I+GWG EDV LY K + S L R+ G+ H++H C L P+QYKMC+

Sbjct: 483 GAGGFDTSIQGWGLEDVDLYNKVILSGLRPFRSQEVGVVHIFHPVHCDPNLDPKQYKMCL 542

Query: 495 QSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSS 529

SKA AS QL L +E HL + +T S

Sbjct: 543 GSKANTFASTMQLAEL---WLEKHLGVRYNRTLS 573

☐ >gi|7959793|gb|AAF71068.1| PRO0082 [Homo sapiens]
Length = 109

Score = 195 bits (496), Expect = 2e-48

Identities = 84/106 (79%), Positives = 95/106 (89%)

Query: 425 MTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPVRGLFHLWHEKRCMDE 484

MTCQYRSDF+ IGGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEKRC DE

Sbjct: 1 MTCQYRSDFLTIGGFDMEVKGWGGEDVHLYRKYLHGD LIVIRTPVPGLFHLWHEKRCDE 60

Query: 485 LTPEQYKMCQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530

LTPEQY+MC+QSKAMNEASH LGMLVFR EIE HL KQ +T+S+

Sbjct: 61 LTPEQYRMCIQSKAMNEASHSHLGMLVFREEIETHLHKQAYRTNSE 106

☐ >gi|38086850|ref|XP_194358.2| similar to mKIAA0990 protein [Mus musculus]
Length = 800

Score = 192 bits (488), Expect = 2e-47

Identities = 107/299 (35%), Positives = 168/299 (56%), Gaps = 21/299 (7%)

Query: 215 RTERDKGTLYELTFKGDHKHEFKRLILFR-PFSPIMKVKNELNMANTLINVIVPLAKRV 273

R +D G+L L+ + K+L+ F+ P S K E IN+++PL+ R

Sbjct: 495 RINQDSGSLSFSL-----NSLKKLVAFQLPGS-----KTEHKPEKKEKINILIPLSGRF 543

Query: 274 DKFRQFMQNFREMCIEQDGRVHLTVVYFGKE----EINEVKGILENTSKAANFRNFTFIQ 329

D F +FM NF + C+ + V L ++ F + + +V+ + + K + +

Sbjct: 544 DMFVRFMGNFEKTCCLIPNLNVKLVILFNSDSNPDKAKQVELMRDYRVKYPK-ADMQVLP 602

Query: 330 LNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTRCLNTQPGKKVFYPVLFSSQ 389

++G FSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQ

Sbjct: 603 VSGGFSRALALEVGSSQFNNE-LLFFCDVDLVFTAFLQRCRANTVLGQQIYFPIIFSQ 661

Query: 390 YNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDLDIKGWGE 449

Y+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG E
 Sbjct: 662 YDPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLE 718

Query: 450 DVHLYRKYLHSNLIVV RTPVRGLFHLWHEKRCMDELTP EQYKMCMQSKAMNEASHGQLG 508
 DV L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL
 Sbjct: 719 DVDLFNKVVQAGLKTFRSQEVGVVHIHPVVC DPNLDPKQYKMCLGSKASTFGSTQQLA 777

 >gi|37360174|dbj|BAC98065.1| mKIAA0990 protein [Mus musculus]
 Length = 821

Score = 192 bits (488), Expect = 2e-47
 Identities = 107/299 (35%), Positives = 168/299 (56%), Gaps = 21/299 (7%)


Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFR-PFSPIMKVKN EKLNMANTLINIVIVPLAKRV 273
 R +D G+L L+ + K+L+ F+ P S K E IN+++PL+ R
 Sbjct: 516 RINQDSGSLSLFSL-----NSLKKLVAFQLPGS-----KTEHKPEKKEKINILIPLSGRF 564

Query: 274 DKFRQFMQNFREMCIEQDGRVHLTVVYFGKE----EINEVKGILENTSKAANFRNFTFIQ 329
 D F +FM NF + C+ + V L ++ F + + +V+ + + K + +
 Sbjct: 565 DMFVRFMGNFEKTC LIPNLNVKL VILLFNSDSNPDKAKQVELMRDYRVKYPK-ADMQVLP 623

Query: 330 LNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLF SQ 389
 ++G FSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQ
 Sbjct: 624 VSGGFSRALALEVGSSQFNNES-LLFFCDVDLVFTA EFLQRCRANTVLGQQIYFPPIFSQ 682

Query: 390 YNPGIYGHHDVAPPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGE 449
 Y+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG E
 Sbjct: 683 YDPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLE 739


Query: 450 DVHLYRKYLHSNLIVV RTPVRGLFHLWHEKRCMDELTP EQYKMCMQSKAMNEASHGQLG 508
 DV L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL
 Sbjct: 740 DVDLFNKVVQAGLKTFRSQEVGVVHIHPVVC DPNLDPKQYKMCLGSKASTFGSTQQLA 798

 >gi|18606381|gb|AAH23112.1| Galnact2 protein [Mus musculus]
 Length = 109

Score = 191 bits (486), Expect = 3e-47
 Identities = 81/106 (76%), Positives = 96/106 (90%)

Query: 425 MTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVV RTPVRGLFHLWHEKRCMDE 484
 MTCQY+SDF+++GGFD+++KGWGGEDVHLYRKYLH +LIV+RTPV GLFHLWHEK C DE
 Sbjct: 1 MTCQYQSDFLSVGGFDMEVKGWGGEDVHLYRKYLHGD L VIRT PVPGLFHLWHEKHCAD E 60

Query: 485 LTPEQYKMCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
 LTPEQY+MC+QSKAMNEASH LGM+VFR EIE HLRKQ +T+S+
 Sbjct: 61 LTPEQYRMCIQSKAMNEASHSHLGMMVFREIEHMLRKQAYRTNSE 106

 >gi|47086685|ref|NP 997843.1| carbohydrate (chondroitin) synthase 1; wu:fc27h0
 gi|40352710|gb|AAH64670.1| Carbohydrate (chondroitin) synthase 1 [Danio rerio]
 Length = 801

Score = 187 bits (475), Expect = 5e-46
 Identities = 101/281 (35%), Positives = 159/281 (56%), Gaps = 13/281 (4%)

Query: 234 HEFKRLILFRPFSPIMKVKN EKLNMANTLINIVIVPLAKRVDKFRQFMQNFREMCIEQDGR 293
 + K L+ F+ SP ++ K IN++VPLA R + F +FM NF ++C+ +
 Sbjct: 507 NSLKMLVPFKLSSPGIEQH EPK---EKKINILVPLAGRYEIFLR FMANFEKICLIPNQ N 562

Query: 294 VHLTVVYFGK----EEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKG 349
 V L ++ F E I +++ + E K + ++G FSR L+VG+ +
 Sbjct: 563 VKLLILLFSTDNNTERIKQIELMREYRMKY PK-ADMEIKPVSGPFSRALALEVGSAHFT- 620

Query: 350 SNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLF SQYNPGIYGHHDVAPPPLEQQ L 409
 ++ LLF+CDVD+ FT +FL CR NT G++ ++P++FSQY+P ++Y P +


Sbjct: 621 NDSLLFYCDVDLLFTPDFLTRCRGNTILGEQTYFPPIIFSQYDPKVVA---GKVPSDNHY 677

Query: 410 VIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVTRTPV 469
V +TG WR +GFG+ C Y+ D + GGFD+ I+GWG EDV L+ K++ S + + R+

Sbjct: 678 VFTSKTGLWRHYGFGIVCVYKGDVKGAGGFDVSIQGWGLEDVDLNFNKFVQSGIKLFRSTD 737

Query: 470 RGLFHLWHEKRCMDELTPSEQYKMCMSKAMNEASHGQLGML 510
G+ H+ H C L P+QYKMC+ SKA + S QL L

Sbjct: 738 TGIVHVHPVVCDPNLDPKQYKMCCLGSKASSHGSTQQLAEL 778

 >gi|47213615|emb|CAF95956.1| unnamed protein product [Tetraodon nigroviridis]
Length = 838

Score = 186 bits (473), Expect = 9e-46

Identities = 96/252 (38%), Positives = 143/252 (56%), Gaps = 9/252 (3%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK---EEINEVGILENTSK 318
+N++VPL+ R D F +FM NF +C+ + V L V+ F E + +V+ + E K

Sbjct: 570 VNILVPLSGRYDIFVRFMANFERICLIPNQNVKLLVLLFNTDNTERVKQVELMREYHMK 629

Query: 319 AANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPG 378
+ G FSR L+VG+ + ++ LLF+CDVD+ FTSEFL CR NT G

Sbjct: 630 YPR-AEMEIRPVTGFSFRRALALEVGSLSHFS-NDSLLFYCDVDLLFTSEFLKRCRANTALG 687

Query: 379 KKVFPVPLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGG 438
+ ++P++FSQY+P ++Y P V +TG WR++GFG+ C Y+ D + GG

Sbjct: 688 AQAYFPPIIFSQYDPKVVA---GKVPSNNHYVFTAKTGLWRNYGFGIVCVYKGDVLRAGG 744

Query: 439 FDLDIKGWGGEDVHLYRKYLHSNLIVVTRPVRGLFHLWHEKRCMDELTPSEQYKMCMSKA 498
FD I+GWG EDV L+ K++ S + + R+ G+ H+ H C L +QYKMC+ SKA

Sbjct: 745 FDTSIQGWGLEDVDLNFNKFVQSGIKLFRSTDGTGIVHIHPVICDPNLEAKQYKMCCLGSKA 804

Query: 499 MNEASHGQLGML 510
+ S QL L

Sbjct: 805 SSHGSTQQLAEL 816

 >gi|40789012|dbj|BAA76834.2| KIAA0990 protein [Homo sapiens]
Length = 883

Score = 186 bits (473), Expect = 9e-46

Identities = 106/297 (35%), Positives = 169/297 (56%), Gaps = 17/297 (5%)

Query: 215 RTERDKGTLTYELTFKGDHKEFKRLILFRPFSPIMKVKNKLNLMANTLINVIVPLAKRVD 274
R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D

Sbjct: 577 RINQESGSLSLFSL-----NSLKKLVFPQ---LPGSKSEHKEPKDKKINILIPLSGRFD 626

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKEE-INEVGILENTSKAANF--RNFTFIQLN 331
F +FM NF + C+ + V L V+ F + ++ K + T + + + ++

Sbjct: 627 MFVRFMGNFEKTCCLIPNQNVKLVLLFNSDSNPDKAKQVELMTDYRIKYPKADMQILPVS 686

Query: 332 GEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFPVPLFSQYN 391
GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY+


Sbjct: 687 GEFSRALALEVGSSQFNNE-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPPIIFSQYD 745

Query: 392 PGIIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGEDV 451
P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG EDV

Sbjct: 746 PKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGDVLRVGGFDVSIQGWGLEDV 802

Query: 452 HLYRKYLHSNLIVVTRPVRGLFHLWHEKRCMDELTPSEQYKMCMSKAMNEASHGQLG 508
L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL

Sbjct: 803 DLFNKVVQAGLKTFRSQEVGVVHVHPVFCDPNLDPKQYKMCCLGSKASTYGSTQQLA 859

 >gi|15617453|dbj|BAB64936.1| chondroitin synthase [Homo sapiens]
Length = 802

Score = 186 bits (472), Expect = 1e-45

Identities = 106/297 (35%), Positives = 169/297 (56%), Gaps = 17/297 (5%)


Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274
 R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D
 Sbjct: 496 RINQESGSLSFSL-----NSLKKLVPFQ----LPGSKSEHKEPKDKKINILIPLSGRFD 545

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKEE-INEVKGILENTSKAANF--RNFTFIQLN 331
 F +FM NF + C+ + V L V+ F + ++ K + T + + + ++
 Sbjct: 546 MFVRFMGNFEKTCCLIPNQNVKLVLVLLFNSDSNPDKAKQVELMTDYRIKYPKADMQILPVS 605

Query: 332 GEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQYN 391
 GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY+
 Sbjct: 606 GEFSRALALEVGSSQFNNE-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYD 664

Query: 392 PGIIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCCQYRSDFINIGGFDDLKIGWGGEDV 451
 P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG EDV
 Sbjct: 665 PKIVY---SGKVPNDHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLEDV 721

Query: 452 HLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508
 L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL
 Sbjct: 722 DLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMCCLGSKASTYGSTQQLA 778

 >gi|31542309|ref|NP_055733.2| carbohydrate (chondroitin) synthase 1; chondroitin synthase [Homo sapiens]
 gi|28279346|gb|AAH46247.1| Carbohydrate (chondroitin) synthase 1 [Homo sapiens]
 Length = 802

Score = 185 bits (470), Expect = 2e-45

Identities = 106/298 (35%), Positives = 170/298 (57%), Gaps = 19/298 (6%)


Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274
 R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D
 Sbjct: 496 RINQESGSLSFSL-----NSLKKLVPFQ----LPGSKSEHKEPKDKKINILIPLSGRFD 545

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQL 330
 F +FM NF + C+ + V L V+ F + + +V+ + + K + + +
 Sbjct: 546 MFVRFMGNFEKTCCLIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPK-ADMQILPV 604

Query: 331 NGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY 390
 +GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY
 Sbjct: 605 SGEFSRALALEVGSSQFNNE-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQY 663

Query: 391 NPGIIYGHHDVAPPLEQQLVIKKETGFWRDFGFGMTCCQYRSDFINIGGFDDLKIGWGGED 450
 +P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG ED
 Sbjct: 664 DPKIVY---SGKVPNDHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLED 720

Query: 451 VHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508
 V L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL
 Sbjct: 721 VDLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMCCLGSKASTYGSTQQLA 778

 >gi|37132131|gb|AAQ33393.1| CHSY1 [Homo sapiens]
 Length = 802

Score = 185 bits (470), Expect = 2e-45

Identities = 106/298 (35%), Positives = 170/298 (57%), Gaps = 19/298 (6%)


Query: 215 RTERDKGTLTYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274
 R ++ G+L L+ + K+L+ F+ + K+E + IN+++PL+ R D
 Sbjct: 496 RINQESGSLSFSL-----NSLKKLVPFQ----LPGSKSEHKEPKDKKINILIPLSGRFD 545

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQL 330
 F +FM NF + C+ + V L V+ F + + +V+ + + K + + +
 Sbjct: 546 MFVRFMGNFEKTCCLIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPK-ADMQILPV 604

Query: 331 NGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY 390
+GEFSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY
Sbjct: 605 SGEFSRALALEVGSSQFNNES-LLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQY 663

Query: 391 NPGIITYGHDAVPPLQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGED 450
+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG ED
Sbjct: 664 DPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLED 720

Query: 451 VHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508
V L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL
Sbjct: 721 VDLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMC LGSKASTYGSTQQLA 778

 >[gi|34857503](#)|[ref|XP_218759.2](#)| similar to carbohydrate (chondroitin) synthase 1
norvegicus]
Length = 799

Score = 183 bits (465), Expect = 7e-45
Identities = 106/298 (35%), Positives = 168/298 (56%), Gaps = 19/298 (6%)


Query: 215 RTERDKGTLYELTFKGDHKHEFKRLILFRPFSPIMKVKNELNMANTLINVIVPLAKRVD 274
R +D G+L L+ + K+L+ F+ M+ K K IN+++PL+ R D
Sbjct: 495 RINQDSGSLSFLS-----NSLKKLVPPQLPGSKMEHKEPK----EKKINILIPLSGRFD 544

Query: 275 KFRQFMQNFREMCIEQDGRVHLTVVYFGKE---EINEVKGILENTSKAANFRNFTFIQL 330
F +FM NF + C+ + V L ++ F + + +V+ + + K + + +
Sbjct: 545 MFVRFMGNFEKTC LIPNLNVKLIVLLFNSDSNPDKAKQVELMRDYRVKYPK-ADMQVLPV 603

Query: 331 NGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGKKVFYPVLFSQY 390
+G FSR L+VG+ + + LLFFCDVD+ FT+EFL CR NT G++++P++FSQY
Sbjct: 604 SGGFSRALALEVGSSQFSNES-LLFFCDVDLVFTAFLQRCRANTVLGQQIYFPIIFSQY 662

Query: 391 NPGIITYGHDAVPPLQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDLDIKGWGGED 450
+P I+Y P + ++TGFWR++GFG+TC Y+ D + +GGFD+ I+GWG ED
Sbjct: 663 DPKIVY---SGKVPSDNHFAFTQKTGFWRNYGFGITCIYKGD LVRVGGFDVSIQGWGLED 719


Query: 451 VHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMSKAMNEASHGQLG 508
V L+ K + + L R+ G+ H+ H C L P+QYKMC+ SKA S QL
Sbjct: 720 VDLFNKVVQAGLKTFRSQEVGVVHVHHPVFCDPNLDPKQYKMC LGSKASTFGSTQQLA 777

 >[gi|41210270](#)|[ref|XP_210054.3](#)| similar to dJ341D10.1 (novel protein) [Homo sapi
[gi|17736645](#)|[emb|CAD19074.1](#)| dJ341D10.1 (novel protein) [Homo sapiens]
Length = 109

Score = 174 bits (442), Expect = 3e-42
Identities = 77/106 (72%), Positives = 90/106 (84%)

Query: 425 MTCQYRSDFINIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDE 484
MTCQYRSDF+ IG FD+++KGWGGEDVHL +KYLH +LIV+ TPV GLFHLW EKRC DE
Sbjct: 1 MTCQYRSDFLIIGRFDMDEVKGWGGEDVHL CQKYLHGDLIVIWTPVTGLFHLWPEKRCDE 60

Query: 485 LTPEQYKMCMSKAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
LTPEQY+MC+QSKA+NEAS LGMLVFR EIE HL KQ +T+S+
Sbjct: 61 LTPEQYRMCIQSKAINEASRSHLGMLVFREIEIETHLHKQAYRTNSE 106

 >[gi|48139301](#)|[ref|XP_396991.1](#)| similar to chondroitin synthase-like protein [Ap
Length = 1094

Score = 174 bits (442), Expect = 3e-42
Identities = 87/258 (33%), Positives = 146/258 (56%), Gaps = 8/258 (3%)

Query: 260 NTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYF---GKEEINEVKGILENT 316
+ +++ I+PL+ R + FR+F+QN+ E+C+ R L ++ + + N ++E
Sbjct: 549 DKMVHFILPLSGRYEIFRRFLQNYEEICLTSGERTALLIMLYHHRTENSFNRTIDLVERL 608

Query: 317 SKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQ 376

```

      +   I ++G FSR K L+ G      K +N L+ F DVDI FT   L   R+NT
Sbjct: 609 KYKYRSASIDIIPISGTF SRAKALNYGVSR LK--NNDLMLFIDVDIAFTESALYRIRVNTL 667

Query: 377 PGKKVFYPVLF SQYNPGIIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINI 436
      G+++++PV+FSQY+P I+YG D   P      I +   G+WR FGFG+   Y+ D+ ++
Sbjct: 668 LGRQMYFPVVF SQYDPKIVYG--DTKSP--DTFAINEMAGYWRQFGFGIVSLYKQDYKHV 723

Query: 437 GGFDLDIKGWGGEDVHLYRKYLHSLNLI VVRTPV RGLFHLWHEKRCMDELTP EQYKMCMQS 496
      GGF+L I+GWG EDV   Y + + S++ + R   + L H++H+   C   +L+   Q+ MCM +
Sbjct: 724 GGFNLSIQGWGKEDVDFYERVIKSSIKIFRAADKDLVHVYHDVECSKDLSETQWSMCMGT 783

Query: 497 KAMNEASHGQLGMLVFRH 514
      KA   A   L   +++ +
Sbjct: 784 KADTLAGTETLAQMIYEN 801

```

☐ >gi|42662609|ref|XP_378128.1| similar to dJ19N1.1 (novel protein) [Homo sapien
gi|9863541|emb|CAC04141.1| dJ19N1.1 (novel protein) [Homo sapiens]
Length = 93

Score = 149 bits (375), Expect = 2e-34
Identities = 65/90 (72%), Positives = 76/90 (84%)

```

Query: 441 LDIKGWGGEDVHLYRKYLHSLNLI VVRTPV RGLFHLWHEKRCMDELTP EQYKMCMQSKAMN 500
      +++KGWGGEDVHLYRKYL +LIV+R PV GLFHLWHEK C DELTP EQY+MC+QSKAM+
Sbjct: 1   MEVKGWGGEDVHLYRKYL RGLD L I V R N P V P G L F H L W H E K H C A D E L T P E Q Y R M C I Q S K A M D 60

Query: 501 EASHGQLGMLVFRHEIEAHLRKQKQKTSSK 530
      EAS   LGMLVFR EIE HL KQ   +T+S+
Sbjct: 61  EASRSHLGMLVFREEIETHLHKQAYRTNSE 90

```

☐ >gi|31158517|gb|AAC85275.1| chondroitin synthase-like protein [Drosophila melanc
Length = 827

Score = 136 bits (343), Expect = 1e-30
Identities = 85/267 (31%), Positives = 132/267 (49%), Gaps = 32/267 (11%)

```

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK-EEINEVKGILENTSKAAN 321
      I   ++P+A R+   F +F++ +   +C+   +   L VV FG +E+ +   +L +
Sbjct: 522 IVFVLPIAGRLGTFRFLRTYERVCVRGEQHC DLLV V I F G S P D E L G D H L Q L L H D L H A R H V 581

Query: 322 FRNFTFIQLNGEFSRGKGLDVGAR--FWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379
      ++   +IQ +   FSRG   LDV AR   ++   +++LF   DVD+ F   E L   R++TQ GK
Sbjct: 582 YQQVNWIIQRSSAFSRGVALDVAARSSYIRQEDIILFI-DVDMVFVEVETLQVRMHTQRGK 640

Query: 380 KVFPVLF SQYNPGIIYGHHDVPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI--NIG 437
      +V+ P++FSQY+P   G      +   I   E G++R FGFG+   Y+SD +   +I
Sbjct: 641 QVYLPVIFS QYDPQRRSGDAGGSEDEGETPRIDDERGYFRQFGFGICAIYKSDILDEDIN 700

Query: 438 GFDLDIKGWGGEDVHLYRKYLH-----SNLIVVRTPV RG 471
      GFD DI GWG EDV   K +                               L V R P
Sbjct: 701 GFDK D I T G W G L E D V K F L E K I V R V G T R Q R G F L A N T A E L A M D Y N E A A E Q W R R L S V F R A P D P T 760

Query: 472 LFHLWHEKRCMDELTP EQYKMCMQSKA 498
      L H++H+   C   +L   QY MC+ +KA
Sbjct: 761 LVHIYHDISCDVQLDAPQYNMCLGTGA 787

```

☐ >gi|45555191|ref|NP_996440.1| CG9220-PC [Drosophila melanogaster]
gi|45446963|gb|AAS65341.1| CG9220-PC [Drosophila melanogaster]
Length = 863

Score = 136 bits (343), Expect = 1e-30
Identities = 85/267 (31%), Positives = 132/267 (49%), Gaps = 32/267 (11%)

```

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK-EEINEVKGILENTSKAAN 321
      I   ++P+A R+   F +F++ +   +C+   +   L VV FG +E+ +   +L +

```

Sbjct: 558 IVFVLPIAGRLGTFERFLRTYERVCVRGEQHCDDLVLVIFGSPDELGDHLQLLHDLHARHV 617

Query: 322 FRNFTFIQLNGEFSRGKGLDVGAR--FWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379
++ +IQ + FSRG LDV AR + + +++LF DVD+ F E L R++TQ GK

Sbjct: 618 YQQVNWIQRSSAFSRGVALDVAARSSYIRQEDIILFI-DVDMVFEVETLQVRMHTQRGK 676

Query: 380 KVFYPVLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI--NIG 437
+V+ P++FSQY+P G + I E G++R FGFG+ Y+SD + +I


Sbjct: 677 QVYLPVIFSQYDPQRRSGDAGGSEDEGETPRIDDERGYFRQFGFGICAIYKSDILDEDIN 736

Query: 438 GFDLDIKGWGGEDVHLYRKYLH-----SNLIVVRTPVRG 471
GFD DI GWG EDV K + L V R P

Sbjct: 737 GFDKDITGWGLEVDKFLKIVRVGTRQGRFLANTAEAMDYNEAAEQWRRLSVFRAPDPT 796

Query: 472 LFHLWHEKRCMDELTPQYKMCMSKA 498
L H++H+ C +L QY MC+ +KA

Sbjct: 797 LVHIYHDISCDVQLDAPQYNMCLGTKA 823

 >gi|45555180|ref|NP_996439.1| CG9220-PB [Drosophila melanogaster]
gi|22832276|gb|AAF48479.2| CG9220-PB [Drosophila melanogaster]
Length = 608

Score = 135 bits (341), Expect = 2e-30

Identities = 85/267 (31%), Positives = 132/267 (49%), Gaps = 32/267 (11%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGK-EEINEVKGILENTSKAAN 321
I ++P+A R+ F +F++ + +C+ + L VV FG +E+ + +L +

Sbjct: 303 IVFVLPIAGRLGTFERFLRTYERVCVRGEQHCDDLVLVIFGSPDELGDHLQLLHDLHARHV 362

Query: 322 FRNFTFIQLNGEFSRGKGLDVGAR--FWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379
++ +IQ + FSRG LDV AR + + +++LF DVD+ F E L R++TQ GK

Sbjct: 363 YQQVNWIQRSSAFSRGVALDVAARSSYIRQEDIILFI-DVDMVFEVETLQVRMHTQRGK 421

Query: 380 KVFYPVLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFI--NIG 437
+V+ P++FSQY+P G + I E G++R FGFG+ Y+SD + +I


Sbjct: 422 QVYLPVIFSQYDPQRRSGDAGGSEDEGETPRIDDERGYFRQFGFGICAIYKSDILDEDIN 481

Query: 438 GFDLDIKGWGGEDVHLYRKYLH-----SNLIVVRTPVRG 471
GFD DI GWG EDV K + L V R P

Sbjct: 482 GFDKDITGWGLEVDKFLKIVRVGTRQGRFLANTAEAMDYNEAAEQWRRLSVFRAPDPT 541

Query: 472 LFHLWHEKRCMDELTPQYKMCMSKA 498
L H++H+ C +L QY MC+ +KA

Sbjct: 542 LVHIYHDISCDVQLDAPQYNMCLGTKA 568

 >gi|31158514|gb|AA085273.1| chondroitin disaccharide polymerase [Caenorhabditis]
Length = 734

Score = 134 bits (336), Expect = 6e-30

Identities = 82/245 (33%), Positives = 134/245 (54%), Gaps = 10/245 (4%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIE--QDGRVHLTVVYFGKEEINEVKGILENTSKAA 320
+++I+PL R F +F Q+ + +C D V LT+V + E+ E + +E A

Sbjct: 484 LHMIMPLRGAAIFARFAQHLKSICARGGDDLAVALTIVLYSSEDEMENRETIEMLR--A 541

Query: 321 NFRNFTFIQLNG-EFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379
+F T I++ FSRG L GA +N LLFF DVD+ FT + L + NT

Sbjct: 542 SFIPVTVIEMGDVSFSRGVALMRGAETLP-ANALLFFTVDVMDLFTCDALKRIKSNTILNA 600

Query: 380 KVFYPVLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439
++++P++FS+++ + +D + L + G++R FG+G+ Y++D +++GGF

Sbjct: 601 QIYFPVIFSEFSHES-WESENKDL--LADAFHYGRGRGYFRHFGYGLAAMYKADLMDVGGF 657

Query: 440 DLDIKGWGGEDVHLYRKYL-HSNLIVVRTPVRLFLHLWHEKRCMDELTPQYKMCMSKA 498
D I+GWG EDV L+ K + + L V+R P GL H++H C + + Q MC SKA

Sbjct: 658 DTKIEGWGKEDVDLFEKAIAKNGRLRVIRVPEPGLVHIYHPHCDENMPTAQKDMCHGSKA 717

Query: 499 MNEAS 503
+ AS

Sbjct: 718 ASLAS 722

☐ >gi|31044074|dbj|BAC76780.1| chondroitin synthase [Caenorhabditis elegans]
Length = 726

Score = 134 bits (336), Expect = 6e-30

Identities = 82/245 (33%), Positives = 134/245 (54%), Gaps = 10/245 (4%)

Query: 263 INVIVPLAKRVDKFRQFMQNFREMCIE--QDGRVHLTVVYFGKEEINEVKGILENTSKAA 320
+++I+PL R F +F Q+ + +C D V LT+V + E+ E + +E A

Sbjct: 476 LHMIMPLRGRAAIFARFAQHLKSICARGGDDLAVSLTIVLYSSEDEMENRETIEMLR--A 533

Query: 321 NFRNFTFIQLNG-EFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNTQPGK 379
+F T I++ FSRG L GA +N LLFF DVD+ FT + L + NT

Sbjct: 534 SFIPVTVIEMGDVSFSRGVALMRGAETLP-ANALLFFTDVDMFLTCDALKRIKSNTILNA 592

Query: 380 KVFYPVLFSQYNPGIYGHHDVAPPLEQQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGF 439
++++P++FS+++ + +D + L + G++R FG+G+ Y++D +++GGF

Sbjct: 593 QIYFPFIVFSEFSHES-WSENDKL--LADAFHYGRGRGYFRHFGYGLAAMYKADLMDVGGF 649

Query: 440 DLDIKGWGGEDVHLYRKYL-HSNLIVVRTPVRGLFHLWHEKRCMDELTPEQYKMCMQSKA 498
D I+GWG EDV L+ K + + L V+R P GL H++H C + + Q MC SKA

Sbjct: 650 DTKIEGWGKEDVDLFEKAIAKNGRLRVIRVPEPGLVHIYHPHCDENMPTAQKDMCHGSKA 709

Query: 499 MNEAS 503
+ AS

Sbjct: 710 ASLAS 714

Get selected sequences

Select all

Deselect all

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF excluding environmental samples

Posted date: Jun 23, 2004 12:06 AM

Number of letters in database: 619,474,291

Number of sequences in database: 1,866,121

Lambda K H
0.321 0.137 0.410

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 129,716,455

Number of Sequences: 1866121

Number of extensions: 5644366

Number of successful extensions: 16471

Number of sequences better than 10.0: 50

Number of HSP's better than 10.0 without gapping: 25

Number of HSP's successfully gapped in prelim test: 25

Number of HSP's that attempted gapping in prelim test: 16391

Number of HSP's gapped (non-prelim): 65

length of query: 532

length of database: 619,474,291

effective HSP length: 130

effective length of query: 402

effective length of database: 376,878,561
effective search space: 151505181522
effective search space used: 151505181522
T: 11
A: 40
X1: 16 (7.4 bits)
X2: 38 (14.6 bits)
X3: 64 (24.7 bits)
S1: 41 (21.8 bits)
S2: 76 (33.9 bits)